SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name:		Examiner # :	
Art Unit: Phone Phone	Number 30	Serial Number:	DADED DICK E MAIL
Mail Box and Blug Room Location	JH:	Results Format Preferred (circle):	PAPER DISK E-MAIL
If more than one search is sub	mitted, please p	rioritize searches in order of ne	ed. *******************
Include the elected species or structures,	keywords, synonym s that may have a sp	lescribe as specifically as possible the subjus, acronyms, and registry numbers, and coecial meaning. Give examples or relevantims, and abstract.	ombine with the concept or
Title of Invention:			
Earliest Priority Filing Date:		· · · · · · · · · · · · · · · · · · ·	
For Sequence Searches Only Please incl appropriate serial number.	ude all pertinent infor	mation (parent, child, divisional, or issued pa	tent numbers) along with the
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apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosug; graft versus host disease; Sjogrem syndrome; pernicious annemna; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia;
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thrombopenia purpura; insulla dependent diabetes; allergy,
attopy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Humanised anti-Fas Humanised anti-Fas

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This is the amino acid sequence of the PDHM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

"This is the amino acid sequence (see AAM83042) entailed making the manalisation of the murine sequence (see AAM83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host call Escherichia coli pHSHM2 SANK 70198 harbors plasmid pHSHM2 carrying a fusion of the humanised PDHM type HFE7A light chain and bNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6272 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HEFA (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells. Cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fras/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, clarederma, Goodpasture syndrome, Crohn's disease, rheumatodid arthritis, autoimmune haemolytic anaemia, eteritity matchinte antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
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Tohru T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 21; Page 220-221; 292pp; English.
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S, Shin Y,
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/note- "claim 9"
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Masahiko O, Nobufusa
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sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).

ó cch 100.0%; Score 1245; DB 19; 11 Similarity 100.0%; Pred. No. 5.2e-67; 238; Conservative 0; Mismatches 0; Query Match Best Local 8 Matches

Length 238;

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Query Match
Best Local Similarity 100.0%
Matches 238; Conservative

The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antification at a noti-Fas antibody is either the murificanti-human Fas monoclonal antibody HFE7A, or a humanised version of HEE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the England of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, arteriosciences, mycoarditis, cardiomyopathy, arteriosciences, mycoarditis, cardiomyopathy, allored and organ graft rejection. Sequences ABB14772-B14774 and ABB14777 and ABB14777 represent the light chains of several humanised HFE7A-derived anti-Fas Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody, complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy, atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain. Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains 121 tigggtkleikrtvaapsvii<u>sp</u>pgdeqiksgtasvvcllnniypreakvqwkvdnalgs 180 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180 **TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC** 11ght chain, SEQ ID NO:109 Claim 20; Page 103; 139pp; Japanese. 238 AA Humanised anti-Fas antibody AAB14778 standard; Protein; **TFGQGTKLEIKRTVAAPSVFE** 99JP-027830 181 GNSQESVTEQDSKDSTYSLSS 24-NOV-2000 (first entry) 98JP-027688 Chimeric - Mus musculus. Chimeric - Homo sapiens. (SANY) SANKYO CO LTD. WPI; 2000-485645/43. N-PSDB; AAA72177. 238 AA; anti-Fas antibody JP2000169393-A. 30-SEP-1999; 30-SEP-1998; 20-JUN-2000. antibodies AAB14778; Sequence 61 121 g ò g ò g

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anti-allergic; anti-arthritic; anti-direction anti-allergic; anti-direction anti-allergic; anti-arthritic; anti-direction anti-allergic; anti-arthritic; anti-dramatological; immunosuppressive; thyromimetic; anti-heumatic; anti-Fas; nephrotropic; anti-hertality; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Sjorgen's syndrome; crohn's disease; scleroderma; sterility; odopasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuppressive, thyronimetic, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive
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Takahashi T;
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clibibition of ligand binding (I) are used to treat and/or prevent diseases associated with the reas/Fas ligand system, especially systemic lupus erythematosus, Hashingto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, Ecleroderma, Goodpasture syndrome, Crohn's disease, autoinmune hemolytic anemia, Sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephintis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not finduce liver disease, and have reduced risk of inducing a human anti-murinejaminic designed light chain which is used in the method described in the whormion.
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Best Local Similarity 100.088 P:
Matches 238; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNSQESVTEQDSKDSTYSLSS
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238 AA;

Sequence

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Length 238;

DB 19;

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This is the amino acid sequence of the HM type humanised light

chain of murine anti-human Fas monoclonal antibody HFETA.

Humanisation of the murine sequence (see AAM83042) entailed making

P47A and K49R amino acid substitutions; these residues are

conserved in the human light (kappa) chain. Host cell E. coll

pHSCHM17 SANK 73597 harbors plasmid pHSCHM17 carrying a fusion

fragment of the humanised HM type HFETA light chain and DNA

encoding the region of human immunoglobulin kappa chain, and is

methods for producing humanised antibodies by culturing host

cells. Humanised versions of HFETA (see AAW83031-37), like native

HFETA, are capable of inducing apoptosis in abnormal cells

cells. The humanised antibodies are used to evaluate, in animal

models, treatments of diseases that involve Fas/Fas ligand

interactions, and also to treat such diseases, including autoimmune

disease (e.g. systemic lupus erythematosus, Hashimoto's disease,

graft versus host disease, Sigren syndrome, pernicious anaemia,

Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

disease, rheumanisch arthritis, autoimmune haemolytic anaemia,

Allesse, rheumanisch arthritis, autoimmune haemolytic anaemia,

and is a see the sease of the sease of the succious anaemia,

Addison's disease, rheumanisch arthritis, autoimmune haemolytic anaemia,

and sease, rheumanisch arthritis, autoimmune haemolytic anaemia,

and sease, rheumanisch arthritis, autoimmune haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jun O, Kimihisa I;
Tohru T:
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113..121
/label= CDR_L3
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                                                                                            "claim 9"
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25-JUN-1997;
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Gaps
                                                                           METDTILLWVLLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                         0;
                                       Indels
/ Match 99.5%; Score 1239; DB 19; Local Similarity 99.2%; Pred. No. 1.2e-66; nes 236; Conservative 2; Mismatches 0;
                     Best Loca
Matches
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The invention relates to compositions for the prevention or treatment or diseases caused by an ablormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murane anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerists, myocarditis, cardiomyopathy, and organ graft rejection. Sequences ABB14772-B14778 and ABB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas murine; humanised antibody, complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy, atteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain. Preventive or treating agence for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody antibody HFE7A; FERM-BP-5828; Light chain, SEQ ID NO:52. Japanese 238 AA. Claim 20; Page 80-81; 139pp8 98JP-0276883 Humanised anti-Fas antibody AAB14773 standard; Proteins 99JP-027830 Anti-Fas antibody; monoclo 24-NOV-2000 (first entry) Chimeric - Mus musculus Chimeric - Homo saptens. SANY) SANKYO CO LID. WPI; 2000-485645/43. N-PSDB; AAA72125. JP2000169393-A. 30-SEP-1999; 30-SEP-1998; 20-JUN-2000. antibodies AAB14773; AAB14773 RESULT g

Query Match

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15-MAR-1999
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-preparent performance of anti-preparent interpretation of the antimitertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashlmoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; myasthenia gravit; multiple sclerodis; Basedow's disease; sterility; myasthenia gravit; insulin dependent diabetes mellitus; arteriosclerosis; myocarcitis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antitialergic, anti-arthritic, antitizal, immunomodulatory, dermatological, immunosuppressive, thyromimetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                        QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                       TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                          Gaps
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                                                                                                                                                                                                                                                                                                                                        METDTILLWVLLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY
                                                                                                       This invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised anti-Fas antibody HFE7A light chain HM type protein.
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                                        Indels
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                  Pred. No. 1.2e-66; ; Mismatches 0;
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99.2%; Preu
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98JP-0276882.
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                  Local Similarity
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antirheumatic, nephrotrople, antiinfertility, neuroprotective,
antiarteriosclerotic, cardigat and hepatropic activity. (I) induce
apoptosis by binding to cellisurface Fas or inhibit it by competitive
cinhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
clupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
cversus host disease, Sorgens syndrome, pernicious or hypoplastic
anemia, Addison's disease, geleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolyede anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
chibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not Anduce liver disease, and have reduced risk of
inducing a human anti-murine fars, and have reduced risk of
inducing a human anti-murine fars, and have reduced risk of
inducing a human anti-murine fars, and have reduced risk of
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Pred. No. 1.2e-66;
2; Mismatches 0;
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Best Local Similarity 99.28
Matches 236; Conservative
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238 AA.

AAB14774 standard; Proteing

AAB14774 RESULT

DRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120

61 qqkpqqppklliyaasnlesg<u>upd</u>

g δ 염 δ d

QOKPGQAPRLLIYAASNLESG

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This is the amino acid sequence of the MM type humanised light chain of murine anti-human Fas monoclonal antibody HFEFA. E. coli SANK 73697 harbors plasmid phsGwMc carrying a fusion fragment of the humanised MM type HFEFA light chain and DNA encoding the region of humanised MM type HFEFA light chain and DNA encoding the region of humanised bain, and is deposited as FERM BP-6071 (Claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFEFA (see AAW83031-37), like native HFEFA, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in cormal cells. The humanised antibodies are used to evaluate, in cormal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graff versus host disease, Sjogren syndrome, pernicious anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rbemarbid arthritis, autoimmune haemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arterilosclerosis, myocarditis, cardiomyopathy, glomerular neephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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Shin Y, Tohru T;
                   label Mat_protein
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/label= CDR_L3
/note= "claim 9"
                                 21..131
/label= Variable
                                                                                    /label= Constant
                                                                                                                                     note= "claim 9"
                                                                                                                                                                                      note= "claim 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hideyuki H, Hiroko Y,
                                                                                                                                                   74..80
/label= CDR_L2
                                                                                                                 /label- CDR_L1
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97JP-0169088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (SANY ) SANKYO CO LTD.
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N-PSDB; AAV70076.
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25-JUN-1997;
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Masahiko O,
                                                                                                                                                                                                                                                                                                        08-OCT-1998
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 Protein
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Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand, appleats modulator; programmed cell death; autoimmune disease; allergy, atteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.

Humanised anti-Fas antibody light chain, SEQ ID NO:54.

24-NOV-2000 (first entry)

AAB14774;

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The invention relates to compositions for the prevention or treatment or diseases caused by an appermality in the Fas/Fas ligand system containing an anti-Fas antiBody as the active component. The anti-Fas antibody is either the murime attin-human Fas monoclonal antibody HFF7A, or a humanised version of HHF7A containing identical CDRs (complementarity determining regions) to antibody HFF7A, Via its interaction with Fas, the Encloded of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosciens, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies.
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Score 1231; DB 21; Length 238; Pred. No. 3.5e-66;

98.98 98.38

Query Match Best Local Similarity

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Gaps

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Length 238; Indels

Score 1231; DB 19; Pred. No. 3.5e-66; 3; Mismatches 1;

98.9%; ilarity 98.3%; Conservative

Similarity

Matches 234;

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Query Match Best Local 3

Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -

98JP-0276883

(SANY) SANKYO CO LTD. WPI; 2000-485645/43. N-PSDB; AAA72126.

99JP-027830

30-SEP-1999; 30-SEP-1998;

20-JUN-2000.

Chimeric - Mus musculus. Chimeric - Homo sapiens.

JP2000169393-A.

Claim 20; Page 83; 139pp; Japanese.

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                                                                                                                                                                                                                                                                                                                                                                                                                                   Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatold arthritis; graft versus hook disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; anultiple sclerosis; Basedow's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antinifertility, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                       QOKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                                   TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                    0; Gaps
                             METDTILLWVLLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                           181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                               Nakahara K, Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                       Humanised anti-Fas antibody HFE7A light chain MM type protein.
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example reference 14; Page 119-120; 263pp; English.
   1;
 Mismatches
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 Conservative
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Matches 234;
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AAW90924
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antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with thie Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashingto disease, rheumatoid arthritis, graft
versus host disease, Slorgem's syndrome, pernicious or hypoplaatic
anemia, Addison's disease, cleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminat, chronic, viral
(B, C or D) or alcoholic), and transplant rejection (I) selectively
inhibit apoptosis in normal recells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they mimic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-muring antibody response. This sequence represents
a humanised anti-ras antibody HEE7A light chain MM type which is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HFE7A; monoclonal antibody, mouse; Fas; humanised antibody; apoptosis; HFE7A; autolimune disease; Hashimoto's disease; systemic lugus erythematosus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autolimune heemolytic anaemia; myasthenia gravis; multiplesclerosis; Basedow's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.9%; Score 1231; DB 21; Length 238; 98.3%; Pred. No. 3.5e-66; 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombopenia purpura; insulmin dependent diabetes; allergy, arteriosclerosis; myocarditis; cardiomyopathy, glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-Fas humanised antibody HFE7A light chain PDHH type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW83034 standard; Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GNSQESVTEQDSKDSTYSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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'label= Mat_protein

'label= Variable .32..238 'label= Constant 'note= "claim 9"

44..58 /label- CDR_L1

/note= "claim 9"

/label- CDR_L2

/note= "claim 9"

CDR_L3

113...121 /label= C

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08-OCT-1997;
01-APR-1997;
25-JUN-1997;
                                30-MAR-1998;
                                               Masahiko O,
                         AU9859701-A
                            08-OCT-1998
                                                                                                               Sequence
                                             Ś
 Region
     Region
        Region
             Region
                  Region
                                             Akio
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This is the amino acid sequence of the PDHH type humanised light chain of murine anti-human Fas monoclonal antibody HFETA.

This state of the murine sequence (see AAM83042) entailed making DIE, PATA, K49R, H80S, P81R, V82L, E84P, A87F, T89V and R107K amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli pHSHH5 SANK 70398 harbors plasmid pHSHH5 carrying a fusion fragment of the humanised PDHH type HFETA light chain and DNA cells. The humanised antibodies by culturing host deposited as FERM BP-6274 (claimed). The invention provides methods for producing humanised antibodies by culturing host methods for producing humanised antibodies by culturing host methods for producing apoptosis in abnormal cells whereasting Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve FasyFas ligand interactions, and also to treat such diseases, including autoimmune careful or such an animal careful or such and also to treat such diseases, including autoimmune disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, mysathenia gravis, multiple sclerosis, Bascacow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular release.
                                                                                                                                                                                                                    New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 21; Page 218; 292pp; English.
                                                                                                                                                                                                                                                                                                                                        diseases e.g. autoimmune disease, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rejection (all claimed).
Nobufusa
                                                                                     WPI; 1998-543440/47.
N-PSDB; AAV70077.
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Sequence

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Gaps

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Length 238; Indels

Score 1207; DB 19; Pred. No. 9.3e-65; 1; Mismatches 5;

Query Match 96.9%; Best Local Similarity 97.5%; Matches 232; Conservative

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RESULT 11
              AAB14777
                                                                                                                                 Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
                                      97JP-0276064.
97JP-0082953.
97JP-0169088.
         98AU-0059701
                                                                                                  (SANY ) SANKYO CO LTD.
                                                                                                                               Hideyuki H,
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas and anti-Fas anti-Fas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                               11 | LIGOGERICE TRANSPORTING PROCESS OF A STANSON OF THE STANSON O
                                                                                                                           RFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
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LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         light chain, SEQ ID NO:107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AA.
                                                                                                                                              61 qqkpgqaprlliyaasnlesg<u>ap</u>
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Chimeric - Homo sapiens,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashlmoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between
                                                                                                                                                                                                            QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                            121 TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                 Gaps
                                                                             GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                         humanized anti-Fas antibody, useful for treating or preventing lammatory or autoimmune disease, induces apoptosis selectively i
                                                              1 METDTILLWVLLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY
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   Length 238;
                                Indels
Score 1207; DB 21;
Pred. No. 9.3e-65;
l; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Humanised HFE7A designed light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory or autoimmune disease, induces
cells with abnormal Fas-Fas ligand systems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 141-142; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                        AAW90927 standard; Protein; 238 AA
                            1;
96.98;
97.58;
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98JP-0276882.
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                              Matches 232; Conservative
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               Similarity
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Query Match
                Local
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cc Fas and its ligand. The products of the invention have anti-inflammatory, antidiabbelic, anti-allergic, anti-arthritic, antidiab.

cc anti-anemic, antidiabbelic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antimifertility, neuroprotective,

cantiarteriosclerotic, cardiant and hepatropic activity. (1) induce
composed by binding to cell, surface Fas or inhibit it by competitive
inhibition of ligand binding (1) are used to treat and/or prevent
classase associated with the Fas/Fas ligand system, especially systemic
clupus erythematosus, Hashing, algand system, especially systemic
custus host disease, Slorgens syndrome, pernicious or hypoplastic
custus, Addison's disease, geleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
candiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
cerdiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
cerdiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind the described anti-ras antiscenter represents
ca humanised anti-ras antiscention.
cells inducing a human anti-murine manish designed light chain which is used in
the method described in the diverse segment represents
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Pred. No. 9.3e-65;
1; Mismatches 5;
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Best Local Similarity 97.5%
Matches 232; Conservative
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Synthetic.

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This is the amino acid sequence of the HH type humanised light chain of murine anti-human Fas monoclonal antibody HFETA.

Humanisation of the murine sequence (see AAW8304) entailed making P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid substitutions; these residues are conserved in the human light chain (see Farman 1900) that type HFETA light chain and DNA encoding the region of human is manusors plasmid pHSGHH7 carrying a fusion fragment of the humanised HH type HFETA light chain and DNA encoding the region of human collaminosis by culturing host cells. Humanised versions of HFETA antibodies by culturing host cells. Humanised versions of HFETA antibodies by culturing host cells. Humanised versions of HFETA care AAW83031-37), like native HFETA, are capable of inhibiting apoptosis in abnormal cells expressing Fas, and of inhibiting apoptosis in normal models, treatments of diseases that involve Fas/Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus enthemness of a service enthem of the service enthemness of the service enthemness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        logren syndrome, pernicious anaemia, Addison's disease,
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, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Page 199-199; 292pp; English.
                              'label= Sig_peptide
                                               1..238
label- Mat_protein
.ocation/Qualifiers
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S, Shin Y,
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                                                                                               Variable
                                                                                                            132..238
/label= Constant
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/label= CDR_L3
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/label- CDR_L1
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/label=
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Masahiko O, Nobufusa
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N-PSDB; AAV70074.
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 Key
Peptide
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238 AA

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody complementarity determining region; CDR; human Fas; Fas ligand; apoperate modulator; programmed cell death; autoimmune disease; allergy atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for the diseases caused by an abnormality e.g. autoimmune diseases, contains
                                                                                                                                    NFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                                  61 qqkpgqaprlliyaasnlesgqpqrfsgsgsgtdftltisrlepadfavyycqqsnedpr 120
                                                                                                                                                                                                      SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                                                                                                                                                                                                                                                                        TOSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY
                                                                                                      tqspgtlslspgeratlsckasqsvdydgdsymnwy
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0
 Length 238;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised anti-Fas antibody light chain, SEQ ID NO:50.
 5; LL
4.8e-64;
6;
                   Pred. No. 4.86
3; Mismatches
 Score 1195;
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                                                                     96.0%
96.2%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 78-79; 139pps
                                                                                                                                                                                                                                                                                                                                                                                          AAB14772 standard; Protein;
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                                                                                                                                      QOKPGQAPRLLIYAASNLESG
                                                                                                                                                                                                      121 TFGQGTKLEIKRTVAAPSVFT
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Query Match
Best Local Similarity 96.2'
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-Fas antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAA72124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP2000169393-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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Page 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic: antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerodsis; Basedow's disease; sterility; myasthenia gravis; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                                                                                                                                                  QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                                                                              TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                 Gaps
                                                                                                                        1 METDTILLWVLLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                      GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                       This invention describes a novel humanized anti-Fas antibody-like
                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised anti-Fas antibody HFE7A light chain HH type protein.
                                                                    ; DB 21; Length 238; 4.8e-64;
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                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example reference 14; Page 114-115; 263pp; English
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                                                                   Score 1195; DE
Pred. No. 4.8e-
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                      AAW90922 standard; Protein; 238 AA
                                                                    96.0%;
96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0276881.
98JP-0276882.
                                                                                                                                                                                                                                                                                                                                                                                                                                           08-AUG-2000 (first entry)
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                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SANY ) SANKYO CO LTD.
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                                                                 Query Match
Best Local Similarity
Matches 229; Conser
                         238 AA;
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30-SEP-1998;
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 antibodies.
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                           Sequence
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molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
cc apoptosis in cells with a normal system, by inhibiting binding between
Fas and its ligand. The products of the invention have anti-inflammatory,
cn triangulatory, dermatological, immunosuppressive, thyromimetic,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
continheumatic, inghrotropic antiinfertility, neuroprotective,
cn inhibition of ligand binding. (I) are used to treat and/or prevent
cdiseases associated with the Fas/Fas ligand system, especially systemic
clupus erythematosus, Hashingto disease, rheumatoid arthritis, graft
cversus host disease, Sjorgemy s syndrome, pernicious or hypoplastic
conemia, Addison's disease, "Storgemy syndrome, cooppasture syndrome, Conn's
disease, autoimmune hemolytic anamia, sterility, myasthenia gravis,
cardiomyopathy, glomerulomephatis, hepatitis (fulminant, chronic, viral
cdependent diabetes mellitugy allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulomephatis, hepatitis (fulminant, chronic, viral
colls. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they mimic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
cut menthod described in the active and the response. This sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.0% Score 1195; DB 21;
96.2% Pred. No. 4.8e-64;
Live : 3; Mismatches 6;
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Best Local Similarity 96.29
Matches 229; Conservative
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April 24, 2002, 15:10:42 ; Search time 42.08 Seconds (without alignments) 127.276 Million cell updates/sec
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Sequence 153, A
Sequence 153, A
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Sequence 5
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Sequence 3
Sequence 1
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2: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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Compugen Ltd
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US-09-281-505-1
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US-08-887-352B-17
US-08-887-352B-17
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US-08-887-352B-17
US-08-887-352B-17
US-09-109-207C-17
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US-09-049-672A-6
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US-09-296-005-19
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GenCore version
Copyright (c) 1993 - 2000
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Match Length
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Sequence 2, Application PC/TUG9613152
GENERAL INFORMATION:
APPLICANT: Martin, Ulrich, et al.
TITLE OF INVENTON: Anti-selectin antibodies for prevention of multiple organ
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
ADDRESSEE: Felfe & Lynch
ADDRESSEE: Attn: Normanin Hanson
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REGISTRATION NUMBER: 30.046
REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHONE: (212) 688-9200
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1031; DB 5;
Pred. No. 5.6e-81;
                    US-08-477-642B-25
DCT-US3-07832-25
US-07-934-373C-39
US-08-437-642B-39
US-09-171-945-99
US-08-171-945-99
US-08-171-945-99
US-08-171-945-99
US-09-097-171A-2
US-09-097-171A-2
US-09-097-171A-2
US-09-097-171A-2
US-09-097-171A-2
US-09-097-171A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-422-712B-2
US-09-607-756-2
US-09-171-945-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: 1BM PC computer Disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8,953
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/5
FILING DATE: 27-Dec-95
APPLICATION NUMBER: EP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 9
FILING DATE: 19-Sep-95
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 805 Third Avenu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" COR
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TOPOLOGY: linear
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
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Best Local Similarity
FILING DATE:
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                                      201 STLTLSKADYEKHKVYACEVTHÖGLSSPVTKSFNRGEC 238
                                                                  181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.7% Score 1017; DB 3;
88.5% Pred. No. 8.8e-80;
ive 13; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  Sequence 9, Application US/08%66151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard/G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WinPatin (Gengitech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/82495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION DATA: 07/74768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION
NAME: SVOBOGA, CTAIG G.
REGISTRATION NUMBER: 39/044
REFERENCE/DOCKET NUMBER: 90/18P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/66163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
FILING DATE: 26-JAN-1994
FILING DATE: 26-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                          South San Francisco
California
                                                                                                                                                                                                                                                                                                                                  Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9841
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 81.7
Best Local Similarity 88.5
Matches 193; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
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STREET: 1
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                                                                                                                                                          US-08-466-151-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCE: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                 81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIKRTVAAPSVF 140
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    Gaps
                                      DIOMIOSPSSLSASVGDRVIITCKASQSVDYDGDSYMNWYQQKPGKAPKLLIYAASNLES
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  Indels
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  11;
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88.5%; Pred. No. 8.8e-80;
                                                                                                                                                                                                                                                                                               STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
  11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08887352B Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1.
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650/225-1489
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Amino Acid
Matches 196; Conservative
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Matches 193; Conservative
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                                                                                Length 218
          ; OTHER INFORMATION: Light chain sequence derived from MAE11 US-09-296-005-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 994; DB 4; Length 21
Pred. No. 8.2e-78;
15; Mismatches 14; Indels
                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Sequence is completely synthesized ; Patent No. 6194551 US-09-282-505-1
                                                                               81.7%; Score 1017; DB 4; 88.5%; Pred. No. 8.8e-80; ive (13; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                201 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                  CCLSSPVTKSFNRGEC 218
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APPLICANT: Esobe Ekinaduese idusogie et al.
TITLE OF INVENTION: POlypeptide Variants
FILE REPERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-51
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/09282505A
; Patent No. 6194551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/09054255
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                                                                                                                                                                                                                                                                                                                                                             STLTLSKADYEKHKVYACEVTE
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LOCATION: 1-218
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                                                                        Query Match
Best Local Similarity 88.59
Matches 193, Conservative
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 LOCATION: 1-218
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US-09-054-255-1
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US-09-282-505-1
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Patent No. 6172213
GEMERAL INFORMATION:
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GEMERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P1123R1
CURRENT PAPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 13
LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides FILE REFERENCE: P1123GLT CURRENT APPLICATION NUMBER: US/09/296,005 CURRENT APPLICATION NUMBER: US/08/887,352 EARLIER APPLICATION NUMBER: US 08/887,352 EARLIER FILING DATE: 1997-07-02 NUMBER OF SEQ ID NOS: 26 SEQ ID NO 13 LENGTH: 218
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                 81 GIPDRESGSGSGTDFTLTIHPVEEEDAATYYCQOSNEDPRTFGQGTKLEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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81.7%; Score 1017; DB 4;
Best Local Similarity 88.5%; Pred. No. 8.8e-80;
Matches 193; Conservative 13; Mismatches 12;
                                                                               201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                               STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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Patent No. 6290957
GENERAL INFORMATION:
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ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Artificial LOCATION: 1-218
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                                                                                                                                                            US-09-109-207C-13
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Length 218; 14; Indels

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EEDAATYYCQQSNEDPRTFGQGTKLEIKRTVAAPSVF 140
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                                                                                                                                                                                             Score 991; DB 2;
Pred. No. 1.5e-77;
                                                                                                                                16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 144 MD f
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                        IFPPSDEQLKSGTASVVCLLNN
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATI
TELEPRA: 650/225-1489
TELEPRA: 650/525-981
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 218 amino acids
Amino Acid
                                                                                              Query Match 79.6
Best Local Similarity 86.2
Matches 188; Conservative
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       ; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-3528-15
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Best Local Similarity
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of TITLE OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                               Query Match 79.8%; Score 994; DB 4; Length 21 Best Local Similarity 86.7%; Pred. No. 8.2e-78; Matches 189; Conservative 15; Mismatches 14; Indels
                                                                                                                                                                                                                                       ; OTHER INFORMATION: E27 anti-1gE antibody light chain US-09-054-255-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                 GENERAL INFORMATION:
APPLICANT: ESONE EXLUADUESE IDUSOGIE ET al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266
                                                                                   CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
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REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225.1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way CITY: South San Francisco STATE: California COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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Patent No. 6242195
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                                                                                                                                                                 LENGTH: 218
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                                                                                                                                                SEQ ID NO 1
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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF SEQUENCES: 26 CORRESPONDENCES: 26 CORRESPONDENCE ADDRESS: ; 0 21 EIVLTQSPGTLSLSPGERATLSGRASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80 ö Score 991; DB 2; Pred. No. 1.5e-77; 44 Mb floppy disk 79.68. Score 991; DB 86.28. Pred. No. 1.5e-tive 16; Mismatches APPLICATION NUMBER: US/08/887,352B FILING DATE: 03-Jul-1997 CLASSIFICATION: 530

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Similarity
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US-08-887-352B-24
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US-09-109-207C-15
                RESULT 11
US-08-887-352B-24
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Patent No. 5994511

GENERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
TUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
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0
                141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                              81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQOSNEDPRTFGQGTKLEIKRTVAAPSVF 140
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 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIKRTVAAPSVF
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; Pred. No. 1.5e-77;
16; Mismatches 14; Indels
                                                                                                                                         STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
                                                                                                                        STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY.
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
medium TYPE: 7.5 inch, 1.64 Mb floppy disk
medium TYPE: 7.5 inch, 1.64 Mb floppy disk
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APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 19:
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86.2%;
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                       STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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LENGTH: 218 amino acids
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Best Local Similarity 86.2%
Matches 188; Conservative
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US-08-887-352B-19
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conard G. Presta, Paula M. Jardieu, John Lowe
Anti-1gE Antibodies and Method of Improving Polypep
                            and Anti-IgE Antibodies and Method of
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1998-06E30
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 87352B
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                                                                                                                                                                                                                                                                                       SOFTWARE: Winderin (General
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION;
REGISTRATION NUMBER: 39/04
                              GENERAL INFORMATION:
APPLICANT: Henry B. LOWMEDS
TITLE OF INVENTION: IMPROVE
TITLE OF INVENTION: IMPROVING
Sequence 24, Application US/086
Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.6%
86.2%
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GENERAL INFORMATION: APPLICANT: Henry B. Lowman, E. TITLE OF INVENTION: Improved FILE REFERENCE: P1123R1
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 3 COMPUTER: IBM PC COMPACUOPER: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 IFPPSDEQLKSGTASVVCLLN
                                                                                                                                                              CITY: South San Francis
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMAT
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
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CURRENT FILING DATE: 1998-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 188; Conservative
                                                                                                                                Genentech,
                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                               ADDRESSEE: Genent
STREET: 1 DNA Way
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OTHER INFORMATION: Light chain F(ab)'2 sequence derived from MAE11
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Patent No. 6172213
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ORGANISM: Artificial
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Best Local Similarity
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US-09-109-207C-24
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CTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-15
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US-09-109-207C-17
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86.2%; Pred. No. 1.5e-77;
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86.2%; Pred. No. 1.5e-77;
live 16; Mismatches 14
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   US 60/051,554
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Patent No. 617213
BERERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard
PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 1997-07-03 NUMBER OF SEQ ID NOS: 44 SEQ ID NO 15 LENGTH: 218
                                                                                                                                                                                                                                                      Best_Local Similarity 86.2
Matches 188; Conservative
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Best Local Similarity 86.2'
Matches 188; Conservative
                                                                                 TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: Artificial
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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Geonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06,30
PRIOR PILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 44
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Anti-IgE Antibodies and Method of Improving Polypept
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 1-218 
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11 
US-09-109-207C-19
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86.28; Pred. No. 1.5e-77;
1ve 16; Mismatches 14
                                         GLSSPVTKSFNRGEC
                                                                                 GLSSPVTKSFNRGEC
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US-09-109-207C-24
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0; Gaps ; 0 Ouery Match 79.6%; Score 991; DB 4; Length 218; Best Local Similarity 86.2%; Pred. No. 1.5e-77; Matches 188; Conservative 16; Mismatches 14; Indels STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 201 181 g g q ç ò ò a ογ

Search completed: April 24, 2002, 15:10:42 Job time: 145 sec

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protein search, using sw model OM protein

April 24, 2002, 15:11:38 ; Search time 49.97 Seconds (without alignments) 362.809 Million cell updates/sec Run on:

US-09-499-662-109 1245

1 METDTILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_68:* l: pir1:*): pir2:* :: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description SUMMARIES \$68212 \$68212 \$01320 \$16112 JL0029 \$68241 JC5810 A56169 A31790 \$14237 \$33161 PC4203 \$38865 JE0244 JE0243 A23746 JE0241 S06084 \$25058 \$52028 \$42772 S52059 S29593 A20969 A49633 PL0106 PT0219 DB Query Match Length 989 684.5 676.5 627 Score Result NO.

KVMSM6 Ig kappa chain pre	Ig kappa chain		Ig	kappa	Ig kappa		Ig	A37927 Ig kappa chain C r	Ig kappa	19	Ig	Ig kappa		kappa chain pr	kappa chain	ALIGNMENTS			nan		Mevision 05-Dec-1998 #text_change 21-Jan-2000		M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shi		A; Description: Structure relationship of kappatype light chains with AL amyloidosis:		
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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		RESULT	JE0242	Ig kappa	C; Species: Homo sapiens (man)	C; Date: 05-Dec-1998	C; Accession: JE0242	R;Alim,	submitt(A; Descr	A; Reference number:	200000

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	77. ilarity 87.	Conservative	SPGTLSLSPGERAT	SPGTLSLSPGERAT	SGSGSGTDFTLTIH	SGSGSGTDFILTIS	EQLKSGTASVVCLL	EQLKSGTASVVCLL	KADYEKHKVYACEVŢ	KADY EKHKVYACEV
	Similarity 87.	0; Conservative	TLTQSPGTLSLSPGERAT	7LTQSPGTLSLSPGERAT	DRFSGSGSGTDFTLTIH	DRFSGSGSGTDFILTIS	PSDEQLKSGTASVVCLL	PSDEQLKSGTASVVCLL	TLSKADYEKHKVYACEVŢ	TESKADYEKHKVYACEV
	atch 77.	190; Conservative	EIVLTQSPGTLSLSPGERATLÄGRASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES	EIVLTQSPGTLSLSPGERAT LS GRASQSVSNNYLAWYQQKPGQAPSLLIYDASSRAT 57	GIPDRESGSGSGTDFTLTIHWGEEDAATYYCOOSNEDPRTFGOGFKLEIKRTVAAPSVF	GIPDRFSGSGSGTDFILTIS	IFPPSDEQLKSGTASVVCLLNNTYPREAKVOMKVDNALQSGNSQESVTEQDSKDSTYSLE		STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC	STLTLSKADYEKHKVYACEV
	ry Match t Local Similarity 87.	ches 190; Conservative	21 EIVLTOSPGTLSLSPGERATISCKASOSVDYDGDSYMNWYQOKPGOAPRLLIYAASNLES 80	1 EIVLTQSPGTLSLSPGERAT	81 GIPDRESGSGSGTDFTLTHEWGEEDAATYYCQQSNEDPRTFGQGTKLEIKRTVAAPSVF 140	58 GIPDRFSGSGSGTDFILTISGÖEPEDFAVYYCQQYDRPPWTFGQGTKVEIKRTVAAPSVF	141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200	118 IFPPSDEQLKSGTASVVCLL	201 STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238	178 STLTLSKADYEKHKVYACEVTHÖGLSSPVTKSFNRGEC 215
	Ouery Match 77.8% Score 968.5; DB 2; Best Local Similarity 87.2% Pred. No. 6.8e-56;	Matches 190; Conservative	Oy 21 EIVLTQSPGTLSLSPGERAT	Db 1 EIVLTQSPGTLSLSPGERAT	Oy 81 GIPDRFSGSGSGTDFTLTIH	Db 58 GIPDRFSGSGSGTDFILTIS	Qy 141 IFPPSDEQLKSGTASVVCLLI		Qy 201 STLTLSKADYEKHKVYACEVŢ	Db 178 STLTLSKADYEKHKVYACEV

V.region; immunoglobulin homology

A; Accession: JE0012
A; Molecule type: protein
A; Residues: 1-215 < ALIS
A; Superfamily: immunoglobulin
F; 16-91/Domain: immunoglobulin

of k type light chains (VkV) identified in cases of AL Yamaki, S.; Kazi, H Ig kappa chain NIG2 precursor thuman
C; Species: Homo sapiens (man)
C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C; Accession: JE0244
R; Alin, M.A.; Hara, Y.; Hossalph M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; submitted to JIPID, November 1998
A; Description: A new subgroup of K type light chains (VkV) identified in casi A; Reference number: JE0243
A; Accession: JE0244
A; Molecule type: protein
A; Residues: 1-215 <ALI>C; Superfamily: immunoglobulin perpending immunoglobuling ~

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M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain Am37 precursor fiuman C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C; Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C; Accession: JE0041 R; Alim, M.A.; Yamaki, S.; Hossafin, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIPID, November 1908 A; Description: Structure relationship of kappatype light chains with AL amyloidosis: A; Reference number: JE0241 A; Reference number: JE0241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
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                                                                                                                          215;
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A; Residues: 1-216 <ALL7
C; Superfamily: immunoglobulin W Zegion; immunoglobulin homology
F;16-92/Domain: immunoglobulin Nomology <IMM>
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                                                                                                                          Length
                                                immunoglobulin
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Pred. No. 1.3e-49;
                                                                                                                        Score 906.5; DB 2
Pred. No. 6.8e-52;
                                                                                                                                                                                                                                                                                                                                                                              19; Mismatches
                                                                                                                                                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           SLSSPVTKSFNRGE
                                           C;Superfamily: immunoglobulin V region; immun C;Keywords: heterotetramer; immunoglobulin F;16-91/Domain: immunoglobulin Domology <IMM>
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78.9%
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                                                                                                                                        Best Local Similarity 85.3
Matches 185; Conservative
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              A; Molecule type: protein A; Residues: 1-215 <LEO>
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A; Reference number: JE0243
A; Reference number: JE0243
A; Rolecule type: protein
A; Residues: 1-215 < ALL>
C; Superfamily: Immunoglobulin V region; immunoglobulin homology
F; 16-90/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.; Kazi,
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                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
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                                                                                                                                                                   GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNE-DPRTFGQGTKLEIKRTVAAPSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #te:
C.Accession: A23746
F.Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of
A;Reference number: A23746; MUID:91131575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                          SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                           933.5; DB 2
No. 1.2e-53;
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82.6%; Pred. No. 5e-52;
ive 12; Mismatches
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<IMM>
                                            Score
Pred.
F;16-90/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain NIG93 precursor - human C; Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Accession: JE0243
R.Alim, M.A.; Hara, Y.; Hossain, N
submitted to JIPID, November 1998
                                         Query Match 75.0%;
Best Local Similarity 84.9%;
Matches 186; Conservative
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Best Local Similarity 82.6°
Matches 181; Conservative
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N;Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C;Accession: 568241; 568214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. Bubmitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrible control of the control of of the control of the
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A; Residues: 1-218 cTAK>
A; Residues: 1-218 cTAK>
A; Residues: 1-218 cTAK>
A; Cross-references: EMBL: D29670; NID: 9473962; PIDN: BAA06141.1; PID: 9473963
B; Takaqi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. FEBS Lett. 375, 273-276, 1995
A; Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A; Reference number: S68211; MUID: 96085223
                                                                                        A)Title: Nucleotide sequence of 13.4 pg 1.2.3. rat myeloma immunoglobulin kappa chain of A)Title: Nucleotide sequence of 13.4 pg 1.2.3. rat myeloma immunoglobulin kappa chain of A)Title: Nucleotide sequence of 12.40 pg 1.2.40 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 PRTFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.8%; Score 794; DB 2; Length 24
62.5%; Pred. No. 1.4e-44;
Live 35; Mismatches 53; Indels
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67.0%; Pred. No. 7.3e-44;
iive 28; Mismatches 44;
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R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
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A; Status: nucleic acid sequence
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Matches 150; Conservative
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A; Residues: 'NI', 3-212 <TAW>
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81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIKRTVAAPSVF 140

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monoclonal antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: JC5810
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a por; A;Reference number: JC5810; Mulp, 98063277
A;Reference number: JC5810
A;Reference number: JC5810
A;Reference number: JC5810
A;Reference number: JC5810
A;Residues: 1-218 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase. It is directed against a i;Superfamily: immunoglobulin Nyregion; immunoglobulin homology <IMM>
F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B.; Rosenbaum, H.; Go.
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Ig kappa chain V region (clone 23.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Jo-Ct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C;Accession: A56169
R;Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum J. Biol. Chem. 270, 6628-6638, 1995
A;Title: Recombinant antibodies in bloactive peptide design.
A;Reference number: A56169; MuID:95204454
IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                 62 VPARFSGSGSGTDFTLNIHPVEKEDVATYYCQHSRELPLTFGAGTKLELKRADAAPTVSI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 IPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIKRTVAAPSVFI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IVLTQSPASLAVSLGQRATISGRASKSVSASGYIYMHWYQQKPGQPPKLLISLASNLESG
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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62.3% Score 776; DB 2;
Best Local Similarity 67.3% Pred. No. 1.8e-43;
Matches 146; Conservative 26; Mismatches 45;
                                                                                                                                                                                                                       60.4%; Score 752; DB 2;
67.5%; Pred. No. 6.1e-42;
ive 28; Mismatches 40;
                                                                                                                                                                                          STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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Best Local Similarity 67.5
Matches 141; Conservative
                               61
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F;36-110/Domain: immunoglobulinghomology <IMM>
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57.98 Pre
tive (199)
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Best Local Similarity
Matches 135; Conserv
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C; Species: Mus musculus (house mouse)
C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C; Accession: S14237
R; Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Rur. J. Blochen. 192, 767-775, 1990
A.Title: Construction and characterization of a recombinant murine monoclonal antibody A; Reference number: S14237
A; Reference number: S14237
A; Molecule type: mRNA
A; Residues: 1-234 cVaN>
A; Residues: 1-234 cVaN>
A; Cross-references: EMBL:X56394; NID:951622; PIDN:CAA39805.1; PID:951623
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: A31790
B; Schulze-Gahmen, U; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.J.
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for a A;Reference number: A92686; MUID:89034213
A;Reference number: A92686; MUID:89034213
A;Reference number: A31790
A;Rolcoule type: mRNA
A;Residues: 1-220 <SCH>
A;Residues: 1-220 <SCH>
A;Residues: 1-220 <SCH>
A;Residues: 1-220 <SCH
A;Residues: 1-220 <SCH
A;Residues: 1-200 <SCH
A;Residues: 1-200
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GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIKRTVAAPSVF
                                                                                                                                                                                                                    IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.5%; Score 716; DB 2;
60.5%; Pred. No. 1.3e-39;
iive 34; Mismatches 51.
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STLTLTKDEYERHNSYTCEATHKTSTSPI 209
                                                                                                                                                                                                                                                                                                                            STLTLSKADYEKHKVYACEVTHQGLSSPV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain V region (17/9) - mouse
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Best Local Similarity
Matches 133; Conserv
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W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C; Accession: S33161
R; Foley, R.C.; Beh, K.J.
Submitted to the EMBL Data Library, July 1990
A; Description: Isolation and characterisation of sheep kappa light chain cDNA. A; Reference number: S33161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_regision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: Pc4203
E;Kwak, J. W.; Lee, D.I.; Choi, E.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, Gene 173, 257-259, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:91364221
                                                                                                                                                                                 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
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                                                                                                      TFGQGTKLEIKRTVAAPSVFIEDPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS
                                                                                                                                                                                                                                                               117 TFGSGTKLEIKRADAAPTVSIBPPSSBQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ
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  Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-230 <FOLD
A;Cross-references: EMBL:X54110; NID:9297103; PIDN:CAA38046.1; FC;Superfamily: immunoglobulin Virejon; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;143-212/Domain: immunoglobulin homology <IMM>
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; DB 2; L
2.6e-39;
ches 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 708.5; DB 2
Pred. No. 4.3e-39;
9; Mismatches 54
Query Match 57.2% Score 712; DB Best Local Similarity 56.3% Pred. No. 2.6e Matches 134; Conservative 37; Mismatches
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us-09-499-662-109.rpr

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RESULT 15
s37484

Ig kappa chain - mouse (fragment)
C; Species: Mus musculus (house-mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C; Accession: S37484
R; Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A; Reference number: S37483
A; Accession: S37484
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-25 cugc.
A; Cross-references: EMBL:X70424 Indianglobulin homology
C; Keywords: heterotetramer; imminoglobulin
C; Keywords: heterotetramer; imminoglobulin
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                                                                                                                                                  A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C;Comment: This protein is specific for human plasma apolitoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an
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   A;Title: Cloning and characterization of CDNAs coding for heavy and light chains of A;Reference number: PC4202; MUID:97082978
A;Accession: PC4203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Mus musculus (thouse mouse)
C; Species: Mus musculus (thouse mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C; Accession: S38865
B; Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A; Description: Combination of a defined specificity and desired isotype by c A; Accession: S38865
A; Status: preliminary
A; Scatus: preliminary
A; Sesidues: 1-219
A; Mindecule type: mRNA
A; Residues: 1-219
A; Mindecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERONGVLNSWTDODSKDSTYSM 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 SGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIKRTVAAPSV 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S:::||:| :| :| |::||::||::||::|| || DVLMTQTPLSLPVSLGDQASISCRSSQSIVHINGNIYLEWYLQKPGQSPKLLIYKVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIVLTQSPGTLSLSPGERATLSCKASQSVDY-DGDSYMNWYQQKPGQAPRLLIYAASNLE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 EIVLTQSPGTLSLSPGERATLSCKASQS-VDYDGDSYMNWYQQKPGQAPRLLIYAASNLE 79
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T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.7%; Score 706.5; DB 2
61.2%; Pred. No. 5.5e-39;
iive 34; Mismatches 50
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S38865
Ig kappa chain - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 59.89
Matches 131; Conservative
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                                                                                              A; Molecule type: mRNA
A; Residues: 1-219 <KWA>
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Gaps
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Length 225;
                                                                         Indels
          54;
DB 2;
Query Match
Best Local Similarity 60.5%, Pred. No. 6.5e-39;
Matches 138; Conservative: 31; Mismatches 54
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15:11:39

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

April 24, 2002, 15:13:47; Search time 29.21 Seconds (without alignments) 298.741 Million cell updates/sec Run on:

US-09-499-662-109 1245 1 METDIILLWVLLLWVPGSTG........EVTHQGLSSPVTKSFNRGEC 238 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 Total number of hits satisfying chosen parameters:

100059 seqs, 36664827 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P01661 mus musculu	P01834 homo sapien	8 mus m	P01665 mus musculu	P01666 mus musculu	P01667 mus musculu	snw	P18135 homo sapien	mus แ	P18136 homo sapien	mus n	P06311 homo sapien	mus แ	P01660 mus musculu	P01662 mus musculu	P01671 mus musculu	P01663 mus musculu	P04207 homo sapien	P01672 mus musculu	P01620 homo sapien	homo	4 homo	homo	3 homo	P01673 mus musculu	P01656 mus musculu	P01659 mus musculu	P06310 homo sapien	P01654 mus musculu	P06313 homo sapien	P04431 homo sapien	P04206 homo sapien	P01655 mus musculu
SUMMARIES	QI	KV3I_MOUSE	KAC_HUMAN	KV3F_MOUSE	KV3M_MOUSE	KV3N_MOUSE	KV30_MOUSE	KV3Q_MOUSE	KV3L_HUMAN	KV3L_MOUSE	KV3M_HUMAN	KV3P_MOUSE	KV3K_HUMAN	KV3R_MOUSE	KV3H_MOUSE	KV3J_MOUSE	KV3S_MOUSE	KV3K_MOUSE	KV3H_HUMAN	KV3T_MOUSE	KV3B_HUMAN	KV3D_HUMAN	KV4C_HUMAN	KV3E_HUMAN	KV3I_HUMAN	KV3U_MOUSE	KV3C_MOUSE	KV3G_MOUSE	KV2F_HUMAN	KV3A_MOUSE	KV4B_HUMAN	KV1W_HUMAN	KV3G_HUMAN	KV3B_MOUSE
	DB -	H	7	Н.		, ,	П	Н	H	-	Н	Н	Н	-	, - 1		-	-	~	H	Н	-	-	Н	Η.	1	Н	-	7	Н	П	٦	7	П
	Query Match Length	131	106	132	111	111	111	111	129	111	129	110	128	111	111	111	111	111	129	111	109	109	134	109	115	111	111	112	133	111	133	129	109	112
di	Query Match	44.2	44.0	42.4	41.4	41.3	41.1	40.9	40.7	40.2	39.6	39.5	36.9	36.4	36.1	35.7	35.7	35.7	35.5	35.3	34.9	34.8	34.6		•	34.2	34.0	33.9	33.9	33.7	33.4	33.3	33.1	33.1
	Score	550	548	528	516	514	512	509	506.5	501	493.5	491.5	459	453	449	445	445	-4	442.5	439	434.5	433.5	431	429.5	427	426	423	422	421.5	420	415.5	414	412.5	412.5
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MEDLINE-72188439; PubMed-502703;

Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

Suter L., The orithody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV The complete amino acid sequence and its significance for the mechanism of antibody production.";

Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
                                                                                           61 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                        61 QOKPGQPPKLLIYLASNLESGVPARFSGSGSRIDFTLIIDPVEADDAATYYCQQNNEDPW 120
                   Gaps
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MEDLINE=71064023; PubMed=5489770;
Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
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Cloned human and mouse Kappa immunoglobulin constant and J region
genes conserve homology in functional segments.";
Cell 22:197-207(1980).
                                                      METDTILLMVLLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY
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Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
Steinmetz-Kayne M., Suter L., Watanabe S.;
(In) Franek F., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press,
New York (1969).
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Gall W.E., Edelman G.M.;
"The covalent structure of a human gamma G-1mmunoglobulin. X.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
                 Indels
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                 13;
   No. 5.1e-38;
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21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
78.6%; Preu. .v..
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                 103; Conservative
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Science 169:56-59(1970).

Science 169:56-59(1970).

MISCELLANBEOUS: THE BUSEQUENCE HAS THE INV (1) ALLOTYPIC MARKER, 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND 83-200.

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SEQUENCE (BENCE-JONES PROTEIN AG).
MEDLINE-69234734; PubMed-1893682;
Titani K., Shinoda T., Puffam F.W.;
The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the Micration of the disulfide bridges.";
J. Biol. Chem. 244:3550-350(1969).
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Sciurognathi; Muridae; Murinae; Mus.
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Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: Tariable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN).
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V -> L (IN INV(1,2) MARKER).

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D -> N (IN REF. 7 AND 8).

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Pred. No. 5.7e-38;
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21-JUL-1986 (Rel. 01, Cremited)
21-JUL-1986 (Rel. 01, Lastifsequence update)
15-JUL-1999 (Rel. 38, Lastifsequence update)
16-JUL-1999 (Rel. 38, Lastifsequence)
Mus musculus (Mouse).
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InterPro; IPR003597; Ig_cl,
Pfam; PF00047; ig; 1.
SMART; SMO407; igc1; 1.
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EMBL; V00557; CAA23823.1;
PIR; A02116; K3HU.
MIM; 147200; -.
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SEQUENCE OF 1-37
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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"Rearrangement of genetic Anformation may produce immunoglobulin
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41.44 Score 516; DB 1; Length 11

Best Local Similarity 87.46 Pred. No. 2.3e-35;
Matches 97; Conservative 7; Mismatches 7; Indels
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86.5%; Pred. No. 3.4e-35;
1ve 3; 8; Mismatches 7;
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21-JUL-1986 (Rel. 01, Last Requence update)
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Nature 276:785-790(1978).

Nature 276:785-790(1978).

InterPro: IPR003006; Ig_MEG.

InterPro: IPR003596; Ig_MEG.

InterPro: IPR003596; Ig_MEG.

SMART: SM00406; IG, Ig_MEG.

Immunoglobulin V region.

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puture 276:785-790(1978).

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InterPro; IPR003506; Ig_MHG.

InterPro; IPR003506; Ig_WHG.

pfam; PF00047; ig; 1.

Immunoglobulin V region.

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Matches 96; Conservative
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-!- MISCELLANGOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROPEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
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MEDILNE-7314024; PubMed-4120629;
MECKean D.J., Potter M., Hood L.E.;
"Mockean immunoglobulin chains. Partial amino acid sequence of a kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 METDTLLLMVLLLWVPGSTGDIVLTQSPASLAVSLGQRATISCRASKSVNTYGNSFNZWY 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                    Burstein Y., Schechter I., "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG KAPPA CHAIN V-III REGION MOI
PRAMEMORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEMORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 528; DB 1; Length 132, Pred. No. 3.1e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A01933; KVMS32.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam: PP00047; ig. 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 7043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.4%; Score 528; DB 69.7%; Pred. No. 3.1e cive 26; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK 4.
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                                                                                                                                                                                                                                          expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                        MEDLINE=78235887; PubMed=98179;
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|121 TFGSGTKLEIKR 132
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132 AA;
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P01665;
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SEQUENCE
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MEDLINE-88171307; PubMed-3027527;
Kipps T.J., Tomhave E., Chan P.P., Carson D.A.;
Autoantibody-associated Rapa 119th chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1098).
-1. DISEASE: THE PROTEIN 189 NOT THE SURFACE IMMUNOGLOBULIN MAUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                            nolo sapteus (mulmun).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Prima<mark>tes</mark>; Catarrhini; Hominidae; Homo.
        03003;
Moh E., Schilling J., Hood L.E.;
Information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                             IG KAPPA CHAIN V-III REGION HAH
                                                                                                                                                                                                                                                                                             Score 509; DB 1; Length 11.
Pred, No. 8.6e-35;
                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING FRAMEWORK 4.
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                                                                                                                                                                                                                                                                       6FAA345279356829 CRC64;
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01-NOV-1990 (Rel. 16, Last Sequence update)
15-JUL-1999 (Rel. 38, Last Annotation update)
IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
                                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                                                                                                                                             BY SIMILARITY
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HSSP; P01789; 2MCP.
InterPro; IPR03306; Ig_MHG;
InterPro; IPR03596; Ig_V5
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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ilarity 85.688
Conservative
                                                                    PIR, E01937; KVMS69.
InterPro; IPR003006; Ig_MHG
InterPro; IPR003596; Ig_Vo
                    Weigert M., Gatmaitan L.,
"Rearrangement of genetic
      MEDLINE-79073152; PubMed-
                                             diversity.";
Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                          Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region.
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SEQUENCE FROM N.A.
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P18135;
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KV3L_HUMAN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                  Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                     GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIK 131
                                                                    81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 512; DB 1; Length 111;
Pred. No. 4.9e-35;
7; Mismatches 8; Indels
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COMPLEMENTARITY-DETERMINING
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                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 6308.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 7769.
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BY SIMILARITY
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86.5%;
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PIR; C01937; KVMSOB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                              STANDARD;
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P01667;
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P01669;
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McKean D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S. 75:3913-3917(1978).
-1- MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR, A01936; KWMSCI.
InterPro; IPR003596; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
FMANEWORK I.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Pred. No. 3.8e-34;
9; Mismatches 8; Indels
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 COMPLEMENTARITY-DETERMINING
JK1 SEGMENT.
BY SIMILARITY.
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Pred. No. 1.7e-34;
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                                          MW; D3C55292772774D0 CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION CBPC 101.
                                                                40.7%; Scur.
75.8%; Pred. No. 1...
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21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
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84.7%;
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Best Local Similarity 75.83
Matches 100; Conservative
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Best Local Similarity 84.7;
Matches 94; Conservative
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129 AA;
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P01664;
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                                                                                                                                                                                                                                                                                                                                  Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light chain variable region gene
"Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-i- DISEASE: THE PROPEIN MATHER PROPEIN MATH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 KAPPA CHAIN V-III REGION PC 7210.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                     Eukaryoria, Metazoa; Chordáta, Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 493.5; DB 1; Length 129; Pred. No. 1.9e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IG KAPPA CHAIN V-III REGION HIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14070 MW; 7395528EA2BB74D6 CRC64;
                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Lastisequence update)
15-JUL-1999 (Rel. 38, Lastisequence update)
IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
                                                                                                                                                                  129 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 39.6%; Score 493.5; lest Local Similarity 74.2%; Pred. No. 1.9e Matches 98; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 AA
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BY SIMILARITY
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BUKEWIA.

PIR; PLO021, K3HUHI.

R HSSP; P01789; 2MCP.

JR InterPro; IPR003506; Ig_MHC.

"-f-m; PF00047; ig; 1.

"-f-m; PF00047; ig; 1.

"MO0406; IGv; 1.

"ON region; Signal.

IG K
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=88171307; PubMed=3127527;
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des mandadays a li
                                                                                                                                                                  STANDARD;
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129 AA;
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                                                                                                                                                                KV3M_HUMAN
P18136;
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NON_TER
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KV3M_HUMAN
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SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                          EIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-86041852; PubMed-2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                       MEDLINE-79073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                       DB 1; Length 110;
                                                                                                                                                                                                                                                                                                                                                                         81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQOSNEDPRTFGQGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                   COMPLEMENTARITY - DETERMINING 1.
                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING 3. FRAMEWORK 4.
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                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                        69F1A5CE886B1249 CRC64;
                                                                                                                                                                                                                                                                                     Score 491.5; DB 1;
Pred. No. 2.2e-33;
8; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
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                                                                                                                                                                                                                                   SIMILARITY
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                                                                                                                                                                                                                                                       MW.;
                                                                                         PIR; D01937; KVMST0.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                     ch 39.5%;
1 Similarity 84.7%;
94; Conservative
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                 276:785-790(1978).
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38
53
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110
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101
23
110
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Best Local Similarity
           NCBI_TaxID=10090;
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P06311;
                                                                          diversity
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SEQUENCE
                                SEQUENCE.
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QQKPGQAPRLLIYAASNLESĞİPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
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                               IG KAPPA CHAIN V-III REGION IARC/BL41.
                                                                                                                                                                                                                                                                              1 METDTILLMVLLLMVPGSTGETWLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mammalia; Eutheria; Rodeneta; Sciurognathi; Muridae; Murinae; Mus
NGBT maxin=10000.
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Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                     ch 36.9% Score 459; DB 1; Length 128; I Similarity 71.2% Pred. No. 1.2e-30; 94; Conservative 11; Mismatches 23; Indels
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Pred. No. 2.9e-30;
L; Mismatches 14; Indels
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                                                                                                              COMPLEMENTARITY-DETERMINING JK1 SEGMENT.
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                                                          COMPLEMENTARITY - DETERMINING
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                                                                                                                                                                            CC8957F0FE3B9012 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last-sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGIQN PC 6684.
                                                                                                                                                  SIMILARITY
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                                              FRAMEWORK 1
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11
                                                                                                                                                                          14070 MW;
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR0030596; Ig_WHG.
Interpro; IPR0030596; Ig_WHG.
Pfam; PF00047; Ig; 1.
SWART; SM00406; IGv; 1.
Immunoglobulin V region.
DOMAIN 24 38
DOMAIN 24 38
DOMAIN 54 60
CC
DOMAIN 61 92
DOMAIN 61 92
DOMAIN 193 101
CC
DOMAIN 193 101
CC
DOMAIN 193 101
CC
DOMAIN 102 111
E
DISULFID 23 92
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NON_TER 111 111
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Best Local Similarity 77.5%;
Matches 86; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diversity.";
Nature 276:785-790(1978).
 Immunoglobulin V region;
                   20
128
43
54
69
76
                                                                                                                                                                                                                                                                                                                                                                                                 121 TFGQGTKLEIKR 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A01938; KVMS84
                                                                                                                                                                                                                                    Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                            128 AA;
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128
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ID KV3R_MOUSE
AC P01670;
                              CHAIN
DOMAIN
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DISULFID
NON_TER
SEQUENCE
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SEQUENCE
                  SIGNAL
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SEQUENCE (TEPC 111).
MEKEAN D.J., Bell M., Potter M.;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
related ...
S.A. 75:3313-3917(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                   80
                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. US.-A. 75:3913-3917(1978).
-!- MISCELLANBOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
PIR; A01934; KVMS37.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfan; PR0047; ig_1.
Immunoglobulin V region.
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                                    EIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE (PC 3741).
MEDLINE-79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                             81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPYTFGGGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.1%; Score 449; DB 1; Length 111; 76.6%; Pred. No. 6.2e-30; 1ve 14; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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21-JUL-1986 (Rel. 01, Last seq
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P01662;
21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                              STANDARD;
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TD KV3H_MOUSE

AC 21-JUL-1986

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DT 21-JUL-1986

DE IG KADPA CHA

IG KADPA CHA

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CC MARMMAIA; EU

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RA WEDLINE=7907

RA WECANISME

RA GIVERILA

CO NATIN

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ID KV3J_M(
AC P01662
DT 21-JUL-
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[1]
SEQUENCE (ABPC 22).
MEDLINE-79012520; PubMed=99744;
MECKEAN D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                       -i- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
PIR; A01935; KVMSM6.
                                                                                                                                                                                                                                                                                             SEQUENCE (PC 9245).
MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 35.7%; Score 445; DB 1; Best Local Similarity 76.4%; Pred. No. 1.3e-29; Matches 84; Conservative 5.14; Mismatches 12
15-JUL-1999 (Rel. 38, Last sequence update) IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245. Mus musculus (Mouse).
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12041 MW;
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                                                                                                                                                                                                                                                                                                                                                                                       276:785-790(1978)
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Search completed: April 24, 2002, 15:13:47 Job time: 324 sec

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us-09-499-662-109.rsp

Q9QYF0 Q99qyf0 mus Q9JL84 Q9J184 mus Q9JNGWS Q9INWS CYPC Q9JL82 Q9JL82 bomo Q9NSD6 Q9NSD6 bomo	Q9D8W4 09G8W4 mus Q9NP29 Q90p29 homo Q90LA6 0991La6 mus Q90529 Q90529 ging Q99LC4 mus	Q9D8L4 Q9d814 mus 008907 008907 mus Q9QX57 mus P97797 mus	09H1U5 099L31 090524	Q99M24 O46631 O46631 Q96631 Q9WTN4	000241 000241 homo 0914V0 0974V0 homo 097710 p97710 rat 099125 mus	Q99JC1 Q9QWIS	ALLGNMENTS	PRT Creat	Last sequence upwate) Last annotation update) 47).	a; Craniata; Vertebrata; Euteleostomi; a; Sciurognathi; Muridae; Murinae; Mus.	the EMBL/GenBank/DDBJ databases.	1, -: FB2B06A0B801330A CRC64;	Score 743.5; DB 11; Length 238;	- C	ILLWYLLLWYDGSTGEIVLTGGSPGTLSLSPGERATLSCKASOSVDY-DGDSYMNWYQQRP 64 : : : : :	GOAPRLLIYAASNLESGIPDPREGGGGGGGTUTIHPVEEEDAATYYCQQSNEDPRIFGQ 124 : : :		SEQLISGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 184	ISRADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 長日: : : : IITRDEYERHNSYTCEATHKISTSPIVKSFNRNEC 238	
298 111 107 111 109 601	130 130 484 267 463	473 509 513	361 468 268	506 509 509	398 372 509 473	105 509		PRELIMINARY; (TrEMBLrel. 17, C	el. MG	oa; Chordata; la; Rodentla;	SEQUENCE FROM N.A. TISSUE-MAMMARY TUMOR; Strausberg R.; Submitted (JAN-2001) to the	A; 26344 M	59.7	ervative	SSTGEIVLTOS : :: : ASSSDVVMTOT	SNLESGIPDRE	APSVEIFPPSOEOLI	GTKLEIKRADAAPTVSIFPPSS	ESVTEQDSKDSTYSLSSTLTISKU :	Utio war i
0 25.7 7 23.9 8 23.1 9 20.0 5 19.1									OI-JON-ZOOI (TIEMBLE 01-JUN-2001 (TEMBLE UNKNOWN (PROTEIN FOR	a; Metazo; Euther: ID=10090	AMMARY TURY R.; rg R.; d (JAN-20	238 AV		137; Conser	WVLLLWVPC : : LVLMFWIP1	PRLLIYAAS 	LEIKRTVA	LEIKRADA	TEQDSKDS: : TDQDSKDS:	
20 320 21 297 22 288 23 249 24 237.5					10 178 11 176 12 175.5 13 175		1.T 1.3.7	099M37; 099M37; 01-JUN-2001	O1-JUN-2 O1-JUN-2 UNKNOWN	Eukaryot Mammalia NCBI_Tax	SEQUENCE TISSUE=M Strausbe Submitte	SEQUENCE	# ;	Matches 13	6 ILL : 1 5 VRL	65 GQA		125 GTK	185 ESV 185 NSW	
							RESULT Q99M37	ID AC D	5588		R R R R		no O	Ma	oy G	Qy	Ão .	qa	Oy Dp	
,	<pre>sw model 5:13:12 ; Search time 86.76 Seconds (without alignments) 401.254 Million cell updates/sec</pre>	GSTGEVTHQGLSSPVTKSFNRGEC 238	rt 0.5	residues	osen parameters: 473505	ummaries				. * 'Q	sults predicted by chance to have a control the score of the result being printed, the total score distribution.	SUMMARIES	Description	Q99m37 mus Q9rla5 mus	Q99m11 mus Q9u178 homo Q9u186 homo	29,180 mus musculu 29,180 mus musculu 29,177 homo sapien 29,183 homo sapien 311,79	251179 10010 Q9u170 homo Q9u185 homo Q9u181 homo		Q9er29 mus Q9j174 mus Q9j178 mus	Q91176 Q95182
GenCore version byright (c) 1993 - 2000	Search time 86.76 Seconds (without alignments) 401.254 Million cell upda	7		.05 seqs, 146272329 residues		Minimum Match 0% Maximum Match 100% Listing first 45 summaries		<pre>SP_human:* sp_invertebrate:* sp_manmal:* cn_mhc.*</pre>		11: sp_rodent:* 12: sp_virus:* 13: sp_vortebrate:* 14: sp_unclassified:*	the number of results predicted by chance to have a than or equal to the score of the result being prined by analysis of the total score distribution.		Query Match Length DB ID	.7 238 11 Q99M37 Q99m37 mus .5 214 11 Q9R1A5 Q9r1a5 mus	.8 235 11 Q99Mil Q99mil mus .7 109 4 Q9UIR6 Q9UIR6 Q9UIR6 Q9UIR6 D000 .1 109 4 Q9UIR6 Q9UIR6 Q9UIR6 D000 .1 109 4 Q9UIR6 D000 .1 100 .1	09j180 mus 09u177 homo 09u183 homo 09u139 homo	7 108 4 290170 Q94179 HONG 7.7 108 4 Q90170 Q94187 bomo 7.7 107 4 091181 homo	5 124 4 Q9UL80 Q9U180 homo 5 106 5 Q9U410 schis	.1 107 11 Q9ER29 Q9er29 mus .7 99 11 Q9JL74 Q93174 mus .6 101 11 Q9JL78 Q93178 mus	.5 97 11 Q9JL76 Q9J176 mus .1 104 11 Q9JL82 Q9j182 mus

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25403 MW; 39807BFE6782A3FB CRC64;
    235 AA;
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SMART; SM00406
    SEQUENCE
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Q9UL78;
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                                                                                                                                                       Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-:-SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 EIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 58.3%; Score 679; DB 11; Length 214; Similarity 58.3%; Pred. No. 2.7e-55; 27; Conservative 34; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002129; AAH02129.1; -.
                                                                                                                                                                                                                                                                                                                                                                  52BA205FDE995E2A CRC64;
                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
MUS MUSGULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        099M11;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:6743).
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                            PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                       PRT;
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InterPro; IPR003600; Ig_like.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 2.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                214 AA; 23922 MW;
                       PRELIMINARY;
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Best Local Simi.
Matches 127;
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOSIORILIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primaţes; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                               125 GTKLEI-KRTVAAPSVFIFPRSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 183
                                                                                                                                                                                                                                                                                                                                 67 APRLLIYAASNLESGIPDRFSGS--GSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQ 124
                                                      Gaps
                                                                                                                            6 LLLVFLHHLTGSCAQLVLTQ-PSSVSTSLGSTAKLPCKA--STGNIGDSYVNWYQQYMGR 62
                                                                                                7 LLWVLLLWVPGSTGEIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQ 66
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                                                                                                                                                                                                                                                                                                                                                                                                                            "Myosin-reactive autoantipodies in rheumatic carditis and normal
                                                   13;
     Length 235;
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                                                   86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA; 11646 MW; SF675C52EC7EE197 CRC64;
  DB 11;
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Score 433.5; DB 1 Pred, No. 1.9e-32;
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Query Match

34.88; Score 433.5;
Best Local Similarity 43.08; Pred. No. 1.9e
Matches 102; Conservative 36; Mismatches
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MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF035036; AAD56272.1; -. HSSP; P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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PF00047; 19; 1.
; SM00406; IGV; 1.
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                   01-MXY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 EIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                        Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 GIPDRFSGSGSGTDFTLTIHPVEEDAATYYCQQSNEDPRTFGQGTKLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 109;
                                                                                                                                                                                                                                                                                                            SEÓUENCE FROM N.A.

BEÓUENCE FROM N.A.

WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

Young D.C.;
                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243325F72C7DAC83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 399.5; DB 4;
Pred. No. 1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA; 11928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF206026, AAF69324.1; -
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.1%;
72.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; PO1789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF035028; AAD56264.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F00047; ig; 1.
SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig;
SMART; SM00406: TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13) Last sequence update)
01-MAY-2001 (TrEMBLrel. 17) Last annotation update)
01-JUN-2001 (TrEMBLrel. 17) Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBELIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordita; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                       01-MAY 2000 (TEMBLIAL). 130 Created)
01-MAY 2000 (TEMBLIAL). 130 Last sequence update)
01-MAY-2000 (TEMBLIAL). 140 Last annotation update)
01-JUN-2001 (TEMBLIAL). 140 Last annotation update)
MYOSIN-REACTIVE IMMUNOSIONE LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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-1- SIMILARITY: TO IMMUNOCIOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                 DGDSYMNWYQQKPGQAPRLLIYAASNLESGIPDRFSGS 89
                                                                                               2 SLAVSLGGRATISCRASESYETY GTSLMQWYQOKPGOPPKLIYAASNVESGVPARFSGS 61
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   odies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-98277139; Pubmed 9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
31.485 Score 391; DB 4; Length 108;
Best Local Similarity 66.103 Pred. No. 6.2e-29;
Matches 74; Conservative: 17; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C06681716C4D16F3 CRC64;
                                                                                                                                                                SQOSNEDPRIFGQGTKLEIK 131
                                                                                                                                                                                                        SQOSRKVPWTFGGGTKLEIK 103
31.600 Score 394; DB 11;
ilarity 71.600 Pred. No. 3.1e-29;
Conservative 15; Mismatches 14;
                                                                                                                                                                                                                                                                                                        108 AA.
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                                                                                                                                                                               62 GSGTDFSLNIHPVEEDDIAMYECQOSI
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InterPro; IPR003006; Ig_Mi
Pfam; PP00047; 19; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                90 GSGTDFTLTIHPVEEEDAARE
                                                                                 30 TLSLSPGERATLSCKASOSY
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                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 AA;
                      Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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SEQUENCE
      Query Match
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Q9UL83;
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81 GIPDRESGSGSGTDFTLTIHRVEEEDAATYYCQOSNEDPRTFGQGTKLEIKR 132
                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF000047; ig; 1.
SMART; SMO0406; IGV; 1.
                                                                                        PRELIMINARY;
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HSSP; P01607; 1REI.
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                                                                                                                                                                                                                                                                                                                                                   InterPro; irrocceptam; Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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NON_TER
SEQUENCE
                                                                  RESULT 10
Q9UL70
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Q9UL85
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                                                       fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                    21 EIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                             Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIKR 132
                                                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                        Query Match 31.1%; Score 387; DB 4; Length 108; Best Local Similarity 69.6%; Pred. No. 1.5e-28; Matches 78; Conservative 10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 108;
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                                                                                                                                                                                           9F9C5A92EBA96EEA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.8%; Score 384; DB 4;
66.1%; Pred. No. 2.8e-28;
iive 13; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
            MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                           108 AA; 11834 MW;
                                                                                                                      Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                  EMBL; AF035031; AAD56267.1;
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035035; AAD56271.1;
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.1%
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
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SEQUENCE FROM N.A.
                                                                                                                                                                              108
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01-MAY-2000 (TIEMBLIEL. 13, Created)
01-MAY-2000 (TIEMBLIEL. 13, Last sequence update)
01-MAY-2001 (TIEMBLIEL. 17, Last annotation update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOGULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UL85;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantipodies in rheumatic carditis and normal fetus."
Immunol. Immunopathol. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 EIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primațes; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 GIPDRESGSGSGTDFTLTIHEVEEEDAATYYCQQSNEDPRIFGQGTKLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 30.7%; Score 382; DB 4; Length 108; I Similarity 63.4%; Pred. No. 4.2e-28; 71; Conservative [17; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

**MEDLINE-98277139; PubMed-9614934;

Wu X., Liu B., Van der Merse P.L., Kalis N.N., Berney S.M.

Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primațes, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 AA.
108
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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RA SONG X.T., Feng Z.O., Qiu.Z.N., Li Y.O., Huang H.L., Guan X.H.;
RA SONG X.T., Feng Z.O., Qiu.Z.N., Li Y.O., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC -SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC -DOMAIN.
CR EMBL, AF207620; AAF19434.1;
CR EMBL, PRO0065 19_MM.
CR EMBL, REPPRO; IPR003596; 19_MM.
CR InterPro; IPR003596; 19_MM.
CR InterPro; IPR003596; 19_MM.
CR SWART; SM00406; IGV; 1.
CR SWART; SM00406; IGV; 1.
                                                                                                                                                                                                                       Q9UL80

Q9UL80

Q9UL80

Q9UL80

Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

Q1-MY-2000 (TrEMBLrel. 13, Last annotation update)

MYOSIN-REACTIVE IMMUNGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

HOMO Sapiens (Human)

MAGMMALIa: Butheria: Cordiata: Vertebrata: Euteleostomi:

MAMMMALIa: Butheria: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clin. Immunol. Immunopathel. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigetadia; Schistosomatoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 EIVLTQSPGTLSLSPGERATESCKASQSVDY-DGDSYMNWYQQKPGQAPRLLIYAASNLE 79
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC, MANTEDDY NP30 IMMUNOGLOBULIN LIGHT CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 SGIPDRFSGSGSGTDFTLTIRPVEEEDAATYYCQQSNE-DPRTFGQGTKLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 28.5%; Score 355; DB 4;
1 Similarity 59.6%; Pred. No. 1.5e-25;
68; Conservative 4:20; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=98277139; PubMed=9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF035034; AAD56270.1; InterPro; IPR003006; Ig_MHC. InterPro; IPR003506; Ig_WF Ffam; PF00047; Ig; 1. SMART; SM00406; IGV; 1.
Non-stand of the land of the land
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 68; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6182;
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NON_TER
SEQUENCE
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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.7%; Score 369.5; DB 4; Length 107; ilarity 63.4%; Pred. No. 6.1e-27; Conservative 19; Mismatches 17; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.4%; Score 378.5; DB 4; Length 109; 69.0%; Pred. No. 9.1e-28; Live 10; Mismatches 20; Indels 5
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MEDLINE-99277139; Pubmed-9614934;
WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                      109 109 109 109 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
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                                                                                                                                                                                                                                        EMBL, AD36029; AAD56265.1; -. HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
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HSSP; P80362; 1MT.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SWART; SMO0406; IGV; 1.
NON_TER
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107 AA;
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Matches 78; Conserv
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Best Local Simi
Matches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
SEQUENCE
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SEQUENCE
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Q9UL81
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RESULT Q9UL80

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Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Submitted (MAY 2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                  EIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Musinae; Musinae, Musin
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SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Construction and sequencing of the single-chain antibody gene of human TNF-alpha specific monoclonal antibody.";
Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
                                                                                                                                                                                  ..
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                                                                                                                     DB 5; Length 106;
                                                                                                                                                                                                                                                                                                                                               81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTKLEIK 131
                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEWBLrel. 16, Last Sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.1%; Score 338; DB 11; Length 107; 59.8%; Pred. No. 5.1e-24; tive 16; Mismatches 25; Indels ;
                                                                                                                                                                            Indels
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11478 MW; F20F544426BAE63E CRC64;
                                                                                                               Query Match 28.5%; Score 354.5; DB 5; Best Local Similarity 63.1%; Pred. No. 1.5e-25; Matches 70; Conservative 12; Mismatches 24;
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01-WAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF262753; AAG23804.1;
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Best Local Similarity 59.89
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
106 1
106 AA;
NON_TER
SEQUENCE
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Search completed: April 24, 2002, 15:13:12

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - protein search, using sw model
Run on: April 24, 2002, L5:08:17; Search time 85.18 Seconds (without alignments) 206.967 Million cell updates/sec
Title: US-09-499-662-50 Perfect score: 1242 Sequence: 1 METDIILLWVLLLMVPGSTGEVTHQGLSSPVTKSFNRGEC 238
Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched: 522463 segs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463
Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database: A_Geneseq_1101:* SIDSB/gcdata/geneseqp/AA1980.DAT:* SIDSB/gcdata/geneseqp/AA1981.DAT:* SIDSB/gcdata/geneseqp/AA1982.DAT:* SIDSB/gcdata/geneseqp/AA1983.DAT:* SIDSB/gcdata/geneseqp/AA1983.DAT:* SIDSB/gcdata/geneseqp/AA1983.DAT:* SIDSB/gcdata/geneseqp/AA1985.DAT:* SIDSB/gcdata/geneseqp/AA1985.DAT:* SIDSB/gcdata/geneseqp/AA1985.DAT:* SIDSB/gcdata/geneseqp/AA1989.DAT:* SIDSB/gcdata/geneseqp/AA1989.DAT:* SIDSB/gcdata/geneseqp/AA1989.DAT:* SIDSB/gcdata/geneseqp/AA1999.DAT:* SIDSB/gcdata/geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqp/Geneseqp/AA1992.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1992.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1992.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqp/Geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqp/geneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyAA1993.DAT:* SIDSB/gcdata/geneseqfyAA1993.DAT:* SIDSB/gcdata/geneseqfyAA1993.DAT:* SIDSB/gcdata/geneseqfyAA1993.DAT:* SIDSB/gcdata/geneseqfyAA1993.DAT:* SIDSB/gcdata/geneseqfyAA1993.DAT:* SIDSB/gcdata/geneseqfyAeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyAeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyAeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyAeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyAeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyAeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyAeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyGeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyGeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyGeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyGeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyGeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyGeneseqp/AA1993.DAT:* SIDSB/gcdata/geneseqfyGeneseqfyAeneseqfyGeneseqfyAeneseqfyGeneseqfyAeneseqfyAeneseqfyGeneseqfyGeneseqfyAeneseqfyAeneseqfyAenes
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	AANG3031 AAB14772 AANG3034 AANG3034 AAB14777 AANG927 AANG923 AANG923 AANG3033 AANG9093
DB	21 21 21 21 21 21 21 21 21
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AAW90928	AAB147	AAW909	AAW909	AAW909	AAY9370	AAY937	AAY937	AAW1350	AAY937	AAY93/	AAW956	AAY852	AAU144	AAU144	AAU1440	AAR333	AAG712	AAY500:	AAW956	AAMSOO	AAB742	AAW738	AAW956	ALIG			238 AA.				HFE7A 1		nouse;]	graft	anaemi	rome; (scleros	-depend	astic an	:		/Qualifiers	Sig_peptide	Mat_protein	ple	+ 0 0	, ;
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This is the amino acid sequence of the HH type humanised light chain of murine anti-human Fas monoclonal antibody HFETA.

Humanisation of the murine sequence (see AAW83042) entailed making b47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli pHSGHH7 SANK 73497 harbors plasmid pHSGHH7 carrying a fusion fragment of the humanised HH type HFETA light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6073 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFETA (see AAW8331-37), like native HFETA, are capable of inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis in abnormal cells expressing Fas, and of inhibiting Fas.Induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease,
                                                                                                                                                                                                                                                                                                                                                                                                           Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page 199-199; 292pp; English.
                                                                                /note= "claim 9"
113..121
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Query Match 100.0%; Score 1242; DB 19; Length 238; Best Local Similarity 100.0%; Pred. No. 3.3e-69; Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 QOKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQOSNEDPR 120

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Ouery Match 100.0% Best Local Similarity 100.0% Matches 238; Conservative

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(complementarity determining regions) to antibody HEETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-114778 represent the light chains of several humanised HFE7A-derived anti-Fas murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemla; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain. The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas and though as the active component. The anti-Fas antibody is either the musine anti-human Fas monoclonal antibody HFE7A, or a humanised version of WHFE7A containing identical CDRs Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains 121 tfgggtrleikrtvaapsvfifppsdeglksgtasvvcllnnfypreakvgwkvdnalgs 180 181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; Humanised anti-Fas antibody light chain, SEQ ID NO:50. Claim 20; Page 78-79; 139pp; Japanese AAB14772 standard; Protein; 238 AA. 99JP-0278301. 98JP-0276883. 24-NOV-2000 (first entry) Chimeric - Mus musculus. Chimeric - Homo saplens (SANY) SANKYO CO LTD. 2000-485645/43. 238 AA; N-PSDB; AAA72124. anti-Fas antibody JP2000169393-A. 30-SEP-1999; 30-SEP-1998; 20-JUN-2000. antibodies AAB14772; Seguence 121 AAB14772 a ò qq q ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, anti-allergic, anti-arthritic, antiviral, antirheumatic, nephrotropic, anti-infinfertility, neuroprotective, antiartexlosclerotic, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                             QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120
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                                                                                                                                                              181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPYTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                      antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                            Humanised anti-Fas antibody HFE7A light chain HH type protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example reference 14; Page 114-115; 263pp; English.
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c inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic clupus errythematosus, Habibinoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myssthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitis, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulomephritis, hepatitis (fulminant, chronic, viral CB, Cor D) or alcoholicy; and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do notifinduce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFE/A light chain HH type which is used in the method described in the invention.
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Matches
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This is the amino acid sequence of the PDHH type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAW83042) entailed making DIE, P47A, K49R, H80S, P81R, W82L, E84P, A87F, T80Y and R107K amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli phSHH5 SANK 70398 harbors plasmid pHEHH5 carrying a fusion fragment of the humanised PDHH type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERW BP-6274 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal models, treatments of diseases that involve FasyFas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, addison's disease, Sjogren syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, attrombopenia purpura and insulin-dependent diabetes), allergies, expression relations, mad also are sclerosis, macedony attrophy arteriosclerosis, myocarditis, cardiomyopathy, glomerular preference of the partitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                Jun O, Kimihisa I;
, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; Page 218; 292pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Nobufusa S, Shin Y,
                                                                                                                                          113..121
/label= CDR_L3
/note= "claim 9"
           132..238
/label= Constant
                                                                       /note= "claim 9"
74..80
/label= Variable
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                                                                                                                                                                                                                                                                                                                                                                                                              Hideyuki H, Hiroko Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myocarditis, hepatitis and AIDS
                                               44..58
/label= CDR_L1
                                                                                                             /label= CDR_L2
                                                                                                                                                                                                                                                                                 98AU-0059701
                                                                                                                                                                                                                                                                                                                97JP-0276064
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97JP-0169088
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                                                                                                                                                                                                                                                                                                                                                                               (SANY ) SANKYO CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-543440/47.
N-PSDB; AAV70077.
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                                                                                                                                                                                                                                                                               30-MAR-1998;
                                                                                                                                                                                                                                                                                                                              01-APR-1997;
25-JUN-1997;
                                                                                                                                                                                                                                                                                                                38-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Masahiko O,
                                                                                                                                                                                                                AU9859701-A
                                                                                                                                                                                                                                             08-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                Akio S,
               Region
                                              Region
                                                                                               Region
                                                                                                                                               Region
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Query Match
Best Local Similarity 98.7³
Matches 235; Conservative

238 AA;

Seguence

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Gaps

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Score 1230; DB 19; Length 238; Pred. No. 1.8e-68; 2; Mismatches 1; Indels 0;

99.08;

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The invention relates to compositions for the prevention or treatment or diseases caused by an incommality in the Fas/Fas ligand system containing an anti-Fas and the system entities a methody as the active component. The anti-Fas antibody is either the muthing anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arteriosclerois, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14772-B14774 and AAB14777-B14778 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Fas antibody, monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rreventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibady
                                                              121 TFGQGTRLEIKRTVAAPSVETFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
              9
                                                                                                                                                                      Humanised anti-Fas antibody light chain, SEQ ID NO:107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Japanese.
                                                                                                                                                                                                                                                                                     238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0278301.
                                                                                                                                                                                                                                                                                  AAB14777 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98JP-0276883
                                                                                                                                                                                                                                                                                                                                                24-NOV-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Homo sapiens.
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N-PSDB; AAA72176.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anti-allergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; hephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; Crohn's disease; scleroderma; sterility; Godgosture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating or preventing e.g. apoptosis selectively in
                                                                                                                                                                                                 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                  121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                Gaps
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                                                                                                              181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                  antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                                                                                       METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY
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    Length 238;
                                           Indels
      DB 21;
Score 1230; DB 21
Pred. No. 1.8e-68;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised HFE7A designed light chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized anti-Fas antibody, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory or autoimmune disease, induces cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 141-142; 263pp; English.
                                         5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW90927 standard; Protein; 238
99.0%;
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                                              Conservative
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                       Local Similarity
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30-SEP-1998;
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                                           235;
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Query Match
Best Local (
                                           Matches
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AAW90927
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AAW90927
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AWW antin
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antiarheumatic, nephrotropic, antianteriosippreserve, injunimental antianteriosippreserve, antianteriosippreserve, antianteriosipprotective, antianteriosic antianteriosic antianteriosic cardiant and hepatropic activity. (I) induce apoptosis by binding to call surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulomephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic); and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They band to be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do nottinduce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HEPAA designed light chain which is used in the method described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dermatological, immunosuppressive, thyromimetic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1230; DB 21;
Pred. No. 1.8e-68;
2; Mismatches 1;
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Best Local Similarity 98.78;
Matches 235; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW83032 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238 AA;
immunomodulatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Peptide

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This is the amino acid sequence of the HW type humanised light chain of murine anti-human Fas monoclonal antibody HFF7A.

Humanisation of the murine sequence (see AAW83042) entailed making P47A and K49R amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell E. coli pHSGHM17 SANK 73597 harbors plasmid pHBSGHM17 carrying a fusion fragment of the humanised HW type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6072 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW8301-37). like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autcimmne classes (e.g. systemic lupus erythematchsus, Hernichous anaemia, addisease, rheumatchia remissioned autoimmus haemolytic anaemia, disease, rheumatchia remissioned autoimmus musuchia remissioned autoimmus musuchia remissioned autoimmus musuchia remissioned autoimmus musuchia remissioned autoimmus au
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eyuki H, Hiroko Y, Jun O, Kimihisa I;
Nobufusa S, Shin Y, Tohru T;
                     11..238
/label- Mat_protein
/label= Sig_peptide
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                                                                                                                                                                                                                                                                                           113..121
/label= CDR_L3
/note= "claim 9"
                                                                  11..131
'label= Variable
                                                                                                       132..238
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                                                                                                                                                                            /label= CDR_L1
/note= "claim 9"
74..80
                                                                                                                                                                                                                                              /label= CDR_L2
/note= "claim 9"
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Masahiko O, Nobufusa S, Shin Y
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97JP-0082953.
97JP-0169088.
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N-PSDB; AAV70075.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-OCT-1997;
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Score 1202; DB 19; Length 238;
Pred. No. 9.4e-67;
96.8%;
97.1%;
Query Match
Best Local Similarity
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antibodies.

ö The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the muther anti-human Fas monoclonal antibody HFE7A, or a humanised version offerment anti-human for dentical CDRs (complementarity determining regions) to antibody HFE7A, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis AIDS and organ graft rejection; Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulogaphritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain. rreventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody QOKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120 121 TFGQGTRLEIKRTVAAPSVRÄFPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQS 180 121 tfgggtrleikrtvaapsvfyfppsdeglksgtasvvcllnnfypreakvgwkvdnalgs 180 Gaps 9 ö Indels Humanised anti-Fas antibody light chain, SEQ ID NO:52. 9 1; Mismatches Claim 20; Page 80-81; 139gp; Japanese. AAB14773 standard; Proteig; 238 AA. 98JP-0276883 99JP-02783 Matches 231; Conservative 24-NOV-2000 (first entry) Chimeric - Mus musculus. Chimeric - Homo sapiens. (SANY) SANKYO CO LTD. WPI; 2000-485645/43. N-PSDB; AAA72125. JP2000169393-A. 30-SEP-1999; 30-SEP-1998; 20-JUN-2000. AAB14773; 61 61 AAB14773 RESULT qq q δλ οg ŏ δ δy qq

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Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antininfertility; neuroprotective; antianfertiosclerotic; hepatotropic; antininfertility; apstemnic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents
                                                                                                                                                               QOKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120
                                                                                                                                                                               TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                         Gaps
                                                                                                     1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                        181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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0
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                                          Length 238;
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                                                                          Indels
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                                            DB 21;
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                                          Score 1202; DB 21 Pred. No. 9.4e-67;
                                                                        1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            AAW90923 standard; Protein; 238 AA
                                          96.8%;
97.1%;
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                                                                        Matches 231; Conservative
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                                                            Similarity
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238
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30-SEP-1998;
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 Sequence
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                                             Query Match
                                                                                                                                                                 61
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continuents in cells with amormal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-diabetic anti-arbhitic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiviral, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antirheumatic, nephrotropic, antiinfertility, neuroprotective, antirheumatic, nephrotropic, antiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated withfilme Fas/Fas ligand system, especially systemic versus host disease, Slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, relatively, pernicious or hypoplastic anemia, addison's disease, thrombopenia purpura, insulin dependent diabetes mellitis, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulomephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholicy and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to bothymuman and murine Fass, so can be evaluated in mormine disease models. (I) act on the active site of Fas i.e. they mimic the native ligand, do noffinduce liver disease, and have reduced risk of inducing a human anti-murine antibody FESA light chair which is used in the method described in the light chain HM type which is used in the method described in the light chain the produced in the method described in the light chain the produced in the method described in the light chair the light chair the light chair the light chain the method described in the light chain the l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1202; DB 21; Length 238; Pred. No. 9.4e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; the applay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HFE7A; monoclonal antibody; mouse; Fas; humanised antibody apoptiosis; HFE7A; autoimmine disease; Hashimoto's disease; systemic lupus erythematogus; graft versus host disease; Sjogren syndrome; pernicious anaemia; Addison's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Best Local Similarity 97.1%; Pred. No. 9.4e
Matches 231; Conservatives 1; Mismatches
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New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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                                                                                                                                                                                                                        Hiroko Y, Jun O,
                                                                                                                                                                                                                                                                                                Claim 21; Page 220-221; 292pp; English.
       Socation/Qualifiers
                    'label= Sig_peptide
                                 /label- Mat_protein
21..131
                                                                                                                                                                                                                             Nobufusa S, Shin Y,
                                              /label= Variable
                                                     132..238
/label= Constant
                                                                                                                  /label= CDR_L3
/note= "claim 9"
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/label = C
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25-JUN-1997;
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                                                                                                                                                                                                                              Masahiko O,
             Peptide
                           Protein
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                                        Region
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Kimihisa I;

This is the amino acid sequence of the PDHM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAR83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host call Escherichia coli pHSHM2 SANK 70198 harbors plasmid pHSHM2 carrying a fusion of the humanised PDHM type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6272 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells.

KFE7A, are capable of inducing apoptosis in abnormal cells. Cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas 199and interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, capable of sydrem Goodpasture syndrome, Crohn's disease, rheumatotid arthritis, autoimmune haemolytic anaemia, etchilit, manaemia, multining has an encountered and sease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatotid arthritis, autoimmune haemolytic anaemia, etchilit, musaethod arthritis, autoimmune haemolytic anaemia, etchilit. sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).

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238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-Fas antibody; monoclonal antibody HFB7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomeruloimphritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
                                                                                                                                           QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120
                                                                                                                                                          TFGQGTRLEIKRTVAAPSVF1FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                              Gaps
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           Length 238;
                                             Indels
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             DB 19;
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Score 1195; DB 13
No. 2,5e-66;
                               Pred. No. 2.5e
3; Mismatches
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           96.28;
96.2$;
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                              Best Local Similarity 96.2
Matches 229; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                       Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenda purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                        61 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                TFGQGTRLEIKRIVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                       Gaps
                                                                                                                                                               1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                       181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                     Length 238;
                                                                                                                    Indels
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                                                                                       Score 1195; DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised HFE7A designed light chain protein #2.
                                                                                                   Pred. No. 2.5e-66;
                                                                                                                    3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAW90928 standard; Protein; 238 AA.
                                                                                     96.2%;
96.2%;
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                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-258930/23.
                                                                                                    Similarity
                                          238 AA;
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30-SEP-1998;
                                                                                                    Best Local Sim
Matches 229;
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                                            Sequence
                                                                                       Query Match
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molecule (I) that, induces apoptosis in cells with an abnormal FassFasco ilgand system, by binding to Fas on the cells with an abnormal FassFasco ilgand system, by binding to Fas on the cells with an abnormal FassFasco ilgand system, by indinibiting binding between a people is a motivated in the products of the invention have anti-inflammatory, anti-anamic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomouppressive, thyronimetic, antidiabetic, antidiffertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce cappropiss by pinding to cells surface Fass or inhibit to propertieve inhibition of ligand binding. (I) are used to treat and/or prevent inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic upus serythematosus, Hamimore disease, rheumatoid arthritis, graft versus host disease, slorgen's syndrome, pernicious or hypoplastic versus host disease, slorgen's sterility, myasthenia gravis, allergy, allergy, atteriosclerosis, myocarditis, cardiomyopathy, glomerulomephritis, hepatitis (fulminant, chronic, viral cells mormal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-marked antibody Hers/A designed light chain which is used in the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TFGQGTRLEIKRTVAAPSVEİFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention describes a novel humanized anti-Fas antibody-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autolmmune haemolytic anaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myasthenia gravis; multipie sclerosis; Basedow's disease;
thrombopenia purpura; insulin-dependent diabetes; allergy;
atopy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.
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Pred. No. 2.5e-66;
3; Mismatches 6;
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Best Local Similarity 96.2%;
Matches 229; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 AA;
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This is the amino acid sequence of the MM type humanised light

C chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli

SANK 73697 harbors plasmid pH8GMM6 carrying a fuaton fragment of the

chain of mutype HFE7A light chain and DNA encoding the region of

human kappa chain, and is deposited as FERM BP-601 (claimed). The

culvarion provides methods for producing humanised antibodies by

culturing host cells. Humanised versions of HFE7A (see AAM80301-37),

like native HFE7A, are capable of inducing apoptosis in abnormal

cells expressing Fas, and of inhibiting Fas-induced apoptosis in

commal cells. The humanised antibodies are used to evaluate, in

animal models, treatments of diseases that involve Fas/Fas ligand

interactions, and also to treat such diseases, including autoimmune

c disease (e.g. systemic lupus erythematosus, Hashimoto's disease,

c disease, creamatoid arthritis, autoimmune haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                         Location/Qualifiers
                                                                                      'label= Sig_peptide
                                                                                                                label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 202; 292pp; English.
                                                                                                                                                                                                      - CDR_L1
                                                                                                                               21..131
/label= Variable
                                                                                                                                                                           Constant
                                                                                                                                                                                                                                                                                         /label= CDR_L3
/note= "claim 9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                    74..80
/label= CDR_L2
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/label= (
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N-PSDB; AAV70076.
               Homo sapiens.
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                           Synthetic.
                                                                     Peptide
                                                                                                  Protein
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Ϋ́ 238

Sequence

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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the mutine anti-human Fas monoclonal antibody HFFTA, or a humanised version of HFFTA containing identical CDRs (complementarity determining regions) to antibody HFFTA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFF7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas Iigand; apptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomeruloipephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
                                                                                                                                                                                                          QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQOSNEDPR 120
                                                                                                                                                           Gaps
                                                                     1 METDTILLMVLLLMVPGSTGBIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
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 Length 238;
                                     Indels
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   DB 19;
                   2.9e-66;
Score 1194; DE
Pred. No. 2.9e-
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                   AAB14774 standard; Protein; 238 AA.
 96.18;
illarity 96.28;
Conservative
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Chimeric - Homo sapiens.
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N-PSDB; AAA72126.
                     Similarity
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   Query Match
Best Local Simi]
Matches 229; (
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                                                                                                                                                                                                    TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                      OOKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120
                                                                                                                                           1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                       181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively icells with abnormal Fas-Fas ligand systems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised anti-Fas antibody HFE7A light chain MM type protein.
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                                                                       Length 238;
                                                                                                 Indels
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                                                                  Score 1194; DB 21;
Pred. No. 2.9e-66;
2; Mismatches 7;
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                                                                    96.1%;
96.2%;
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                                                                  Query Match
Best Local Similarity 96.2
Matches 229; Conservative
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                            238 AA;
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antibodies
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                           Sequence
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rigging system, by Allengue, to read the cell stillate, and pievenes apoptosis in cells with abouts of the invention have anti-inflammatory. Fas and its ligand. The products of the invention have anti-inflammatory. Continenate, anti-diabetic, anti-arthritic, anti-iral.

Continenate, antidiabetic, anti-arthritic, anti-iral.

Continenatic, nephrotropic, antidifertility, neuroprotective, antiarterioscieroric, cardiant and hepatropic activity. (1) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic upus erythematosus, Hashimoto disease, rehumatoid arthritis, graft versus host disease, Slorgen's syndrome, pernicious or hypoplastic conenia, Addison's disease, acleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulopephritis, hepatitis (fulminant, chronic, viral (8, C or D) or alcoholic), and transplant rejection. (I) selectively infinite apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of induced and anti-marian and murine disease, and have reduced risk of induced and anti-mariant anti-mariant and anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant anti-mariant and anti-mariant anti-mariant and anti-mariant and anti-mariant and anti-mariant and anti-mariant and anti-mariant anti-mariant and anti-mariant and anti-mariant and anti-mariant and anti-mariant and anti-mariant and anti-mariant and ö inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFE7A light chain MM type which is used in the method described in the invention. 61 qqkpqqppklliyaasnlesg1pdrfsgsgsgtdftltihpveeedaatyycqqsnedpr 120 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120 121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180 Gaps GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY ö Length 238; le (I) that, induces apoptosis in cells with an abno system, by binding to Fas on the cell surface, and Indels Score 1194; DB 21; Pred. No. 2.9e-66; 2; Mismatches 7; 96.1**%**; 96.2**%**; Conservative 238 AA; Similarity Query Match Best Local Simi Matches 229; Sequence 61 181 181 g δ à QQ à

Search completed: April 24, 2002, 15:09:51 Job time: 94 sec

us-09-499-662-50.rag

us-09-499-662-50.rai

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:08:17; Search time 42.08 Seconds

(without alignments)
127.276 Million cell updates/sec
1242
Sequence: 1242
Sequence: 1242
Searched: 1252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Issued_Patents_AA:*

1: /cgn2_6/ptodata/3/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/3/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/3/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

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6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	13,	6	13,	Sequence 13, Appl	1, A	1,	15,	17,	19,	24,	15,	Sequence 17, Appl	Sequence 19, Appl	24,	15,	17,	19,	24,	26,	6, 4	Sequence 6, Appli	153	Sequence 153, App	153,	_	Sequence 25, Appl
SUMMAKIES	ID	PCT-US96-13152-2	US-08-887-352B-13	US-08-466-151-9	US-09-109-207C-13	US-09-296-005-13	US-09-282-505-1	US-09-054-255-1	•	US-08-887-352B-17	US-08-887-352B-19	US-08-887-352B-24	US-09-109-207C-15	US-09-109-207C-17	US-09-109-207C-19	US-09-109-207C-24	US-09-296-005-15	US-09-296-005-17	US-09-296-005-19	US-09-296-005-24	US-07-916-098A-56	US-09-049-672A-6	US-08-487-550-6	US-08-276-852-153	US-08-899-575-153	US-08-899-575-153	PCT-US95-08743-153	US-07-934-373C-25
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æ	Ouery Match	84.1	83.0	83.0	83.0	83.0	81.2	81.2	80.9	80.9	80.9	6.08	80.9	80.9	80.9	80.9	80.9	80.9	80.9	80.9	78.5	78.1	77.7	6.97	6.92	6.97	6.92	8.92
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, PCT-	MOLI US96	, MOLECULE TYPE PCT-US96-13152-2	YPE: protein	tein				
- R	Query Match	Match	11.10	84.18;	1.00	; DB 5;	Length 218;	
Be	sst L	ocal Si	Local Similarity	06	88	Pred. No. 3.9e-82;		

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Gaps

10;

Matches 198;

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121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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                                                   201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                               DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                          APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P0718P2C1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: WinPatin (Genentech)
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION:

PROR APPLICATION DATA:

APPLICATION NUMBER: 08/466163

FILING DATE: 06-Jun-1995

APPLICATION NUMBER: 08/405617

FILING DATE: 15-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/185899

FILING DATE: 26-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/879495

FILING DATE: 07-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/879495

FILING DATE: 07-MAY-1992

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Patent No. 6037453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: Californ's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881 EINFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 14-AUG-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              650/225-1489
650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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: USA
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                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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US-08-466-151-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                               IPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                           GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                          DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                         21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
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Pred. No. 6.1e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.0%; Sco. 89.4%; Pred. No. 0... 89.4%; Pred. No. 0... 12; Mismatches
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FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/08887352B
Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Svoboda, Craig G.
REGIZTRATION NUMBER: 39,044
REFRENCE/DOCKET NUMBER: P112:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/255-1489
TELEFAX: 650/255-1489
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUWTRY: USA
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Amino Acid
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Best Local Similarity 89.44
Matches 195; Conservative
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MEDIUM TYPE: 3.5 inc
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US-08-887-352B-13
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Gaps

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GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                                                                              Length 218;
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; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Sequence is completely synthesized Patent: No. 6194551
                                                                                              83.0%; Score 1031; DB 4; 89.4%; Pred. No. 6.1e-81;
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                                                                                                                                 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09282505A Patent No. 6194551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09054255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Artificial Sequence LOCATION: 1-218
                                                                                                Ouery Match
Best Local Similarity 89.48
Matches 195; Conservative
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US-09-282-505-1
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Patent No. 6172213

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide CURRENT FILING DATE: 1998-106-30

PRIOR APPLICATION NUMBER: US/09/109, 207C

CURRENT FILING DATE: 1998-06-30

PRIOR FILING DATE: 1999-07-03

NUMBER OF SEO ID NOS: 44

SEO ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTICIANT: Henry 1.

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides FILE REFERENCE: P11.23.02.1r

CURRENT APPLICATION NUMBER: US/09/296,005

CURRENT FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 08/887,352

EARLIER FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 13
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   81 GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.0%; Score 1031; DB 4; Length 218;
89.4%; Pred. No. 6.1e-81;
Live 12; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;. NAME/KEY: Artificial
; LOCATION: 1.218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13
                                                                                              201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                          STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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Patent No. 6290957
GENERAL INFORMATION:
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Best Local Similarity
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; TOPOLOGY: Linear
US-08-887-352B-15
Amino Acid
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US-08-887-352B-17
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US-08-887-352B-17
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Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
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                                                                                                                                                                                                                                                                                                                                        Length 218;
                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                                                                        ; OTHER INFORMATION: E27 anti-IgE antibody light chain US-09-054-255-1
                                                                                                                                                                                                                                                                                                                                    Query Match 81.2%; Score 1008; DB 4; Best Local Similarity 87.6%; Pred. No. 5.7e-79; Matches 191; Conservative 14; Mismatches 13;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
            GENERAL INFORMATION:
APPLICANT: Esche Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266
                                                                                      CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
LENGTH: 218
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FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
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NAME: Svoboda, Craig G
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
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Sequence 17, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                              21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES
                                                                                                                                                                                                                                                                     141 IFPPSDEQLKSGTASVVCLLŅNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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  Length 218;
80.9%; Score 1005; DB 2; Length 2
87.2%; Pred. No. 1e-78;
ive 15; Mismatches 13; Indels
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Pred. No. 1e-78;
5; Mismatches 13; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-D65/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: U3J-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                             STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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87.2%; Pre
tive 15;
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NAME: Syoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1.
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STREET: 1 DNA Way
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CITY: South San Francisco
STATE: California
Query Match
Best Local Similarity 87.28
Matches 190; Conservative
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Amino Acid
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Best Local Similarity
Matches 190; Conserv
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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; Pred. No. 1e-78;
15; Mismatches 13; Indels
                                                                                                                                                 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Winbatin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: US/011-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                         Sequence 19, Application US/08887352B Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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87.2%;
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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COMPUTER READABLE FORM:
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Best Local Similarity
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US-08-887-352B-19
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Sequence 15, Application US/09109207C
Patent No. 6172213
GENERAL INFORMATION
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improyed Anti-1gE Antibodies and Method of Improving Polypep
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
                 Sequence 24, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of NUMBER OF SEQUENCES: 26**
CORRESPONDENCE ADDRESS: **
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                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: 3.5 Inch. 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches 190; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                        Genentech, Inc.
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                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
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STREET: 1 DNA Way
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US-08-887-352B-24
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us-09-499-662-50.rai

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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept FILE REPRENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109, 207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR RELIGATION NUMBER: US 60/051,554
NUMBER OF SEQ ID NOS: 44
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    121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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OTHER INFORMATION: Light chain F(ab) sequence derived from MAEll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 218;
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87.2%; Pred. No. 1e-78;
Live 15; Mismatches 13; Indels
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                                             201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                 181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                    Sequence 19, Application US/09109207C Patent No. 6172213 GENERAL INFORMATION:
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Matches 190; Conservative
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LOCATION: 1-218
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Patent No. 6172213
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVERFICOR: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P1123R1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.9%; Score 1005; DB 4; Length 2 ilarity 87.2%; Pred. No. 1e-78; Conservative 15; Mismatches 13; Indels
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COTHER INFORMATION: Light chain sequence derived US-09-109-207C-15
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    us 60/051,554
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                     1997-07-03
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-07
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 15
LENGTH: 218
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SEQ ID NO 17
                                                                                                   TYPE: PRT
ORGANISM: Artificial
                                                                                                                                             FEATURE:
NAME/KEY: Artificial
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Best Local Similarity
Matches 190; Conserv
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US-09-109-207C-24
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April 24, 2002, 15:08:22; Search time 49.97 Seconds (without alignments) 362.809 Million cell updates/sec

US-09-499-662-50 1242 1 METDTILLWVLLLWVPGSTG.......EVTHQGLSSPVTKSFNRGEC 238 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR_68:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ig kappa chain NIG Ig kappa chain NIG Ig kappa chain V-I Ig kappa chain NIG Ig kappa chain pre Ig kappa chain V r monoclonal antibod Ig kappa chain V r Ig kappa chain (mo Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V C Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig kappa chain pre Ig lambda-like cha Description SUMMARIES JE0242 JE0244 JE0244 JE0241 S06084 S06084 JC5810 JC5810 S14237 PC4237 PC4237 PC4237 S3161 S33161 S33162 S337484 \$42772 \$16112 \$25058 \$01320 JL0029 \$68212 \$72212 \$720593 \$520593 \$720593 Query Match Length DB Score 984.5 9938.5 9238.5 915.5 915.7 736 736 737 718 715.7 715.5 715.5 715.5 715.5 715.5 715.6 88.5 699.5 688.5 682 613 609.5 602.5 574.5 571 571 558.5 Result

Ig kappa chain - h	Ig kappa chain C r	Ig kappa chain pre	Ig kappa chain V r	ti-Sm	kapp	kappa	ligh	kapp	Ig kappa chain C r	kapp	Ig kappa chain C r	kapp	light	Ig kappa chain V r	Ig kappa chain pre
\$20631	КЗНО	КЗНОНА	S20636	S49532	КЗНОНІ	KVMSM6	S4 6369	538643	A37927	KVMS32	S26653	A32274	S29577	A56701	PN0446
a	-	-	~	~	<u>,</u>	Н	C)	~	7	H	Ç	a	~	~	7
145	106	129	128	129	129	131	129	134	66	132	66	129	233	128	140
S	1.1	12.6	42.5	42.2	42.1	42.0	41.8	41.8	41.3	40.9	40.8	40.6	40.5	40.2	40.1
44	4	7													
	548 44		527.5	524.5	523.5	522	519.5	519.5	513	508	507	504.5	503	499	498.

ALIGNMENTS

RESULT

Ig kap C;Spec C;Date C;Acce C;Acce R;Alim Submit A;Desic	Ig kappa chain NIG26 precursor - human C.Species: Homo sapiens (man)
C; DG C; DG C; DG R; Al	DECTES: IIOIIIO SUDTEIIS (IIIII)
Subn	C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
A: De	C;ACCESSION: JB/242, R;ALIM, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinod
A; Re	Submitted to JIII, November 1990 A) Reference number: JE0241
A; Mc	A;Wolecule type: protein
C; St. F; 16	C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-91/Domain: immunoglobulin homology <imm></imm>
N BE	Ouery Match 79.3%; Score 984.5; DB 2; Length 215; Best Local Similarity 88.1%; Pred. No. 4.2e-59; Matches 192; Conservative 10; Mismatches 13; Indels 3; Gaps 1;
Qy	21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80 :
qa Ob	81 GIPDRESGSGGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
Qy	141 IFPPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
Oy Db	201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
RESULT JE0244 19 kaper C; Spec C; Date C; Date C; Alime R; Alime R; Alime A; Desc A; Resesi C; Supec A; Resesi C; Supec	RESULT 2 JEO244 JEO244 Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C;Accession: JEO244 Submitted to JIPID, November 1998 A;Bescription: A new subgroup of k type light chains (VkV) identified in cases of AJ A;Reference number: JEO243 A;Reference number: JEO244 A;Molecule type: protein A;Residues: 1-215 <ali> C;Superfamily: immunoglobulin V region; immunoglobulin homology</ali>

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Gaps

5;

,7e-54; es 19; 3

Length 215;

DB

Score 915.5; Pred. No. 1.7

80

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S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain Am37 precursor - human C; Species: Homos sapiens (man)
C; Species: Homos sapiens (man)
C; Accession: U500341
R; Alin, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JTPID, November 1998
A; Description: Structure relationship of kappatype light chains with AL amyloidosis: A; Reference number: J50241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                                                                                                                                                                                                                           81 GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQOSNEDPRTFGQGTRLEIK-RTVAAPSV
                                                                                                                                                                                                                                                                                                                                                                                                                                              DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES
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                     A; Mccession: JE0243
A; Molecule type: protein
A; Residues: 1-215 <ALI>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
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Residues: 1-216 cALL:
C;Superfamily: immunoglobulin V region;
F;16-92/Domain: immunoglobulin homology
                                                                                                                                                                                                           73.78;
82.68;
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80.7%;
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Matches 181; Conservative
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  A; Reference number: JE0243
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Best Local Similarity
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C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: Ac3746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Cham. 266, 2886-28842, 1991
A;Fitle: The primary structure of the Fab fragment of protein KAU, a monoclc A;Reference number: A23746; MUID:91131575
                                                                                                                                                                                                                                                                                      GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNE-DPRTFGQGTRLEIKRTVAAPSV 139
                                                                                                                                                                                                                                                                                                              FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Accession: A23746
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-215 <LEO>
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                Indels
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                                                                             DB 2;
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                                                                          Score 938.5; DB
Pred. No. 5e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.8%; Score 929.5; DB 86.6%; Pred. No. 2e-55;
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                                                                                                                             10; Mismatches
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     <IWW>
F;16-90/Domain: immunoglobulin homology
                                                                          75.6%;
                                                                                                                             Matches 186; Conservative
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nes 188; Conserv
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Best Local Si
Matches 188;
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Gaps

<u>``</u>

25; Indels

Score 885; DB 2; Pred. No. 1.9e-52;

immunoglobulin homology <IMM>

140

58

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24

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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: JC5810
C; Accession: JC5810
R; Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada Biochem. Biophys. Res. Communi 240, 566-572, 1997
A; Title: Structural characterization of mouse monoclonal antibody 13-1 against a por A; Reference number: JC5810; MujD: 98063277
A; Reference number: JC5810
A; Molecule type: protein
A; Residues: 1-218 <AKA>
C; Comment: This catalytic antibody has peroxidase oxidase. It is directed against a C; Superfamily: immunoglobuling region; immunoglobuling region; immunoglobuling viewns.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.24; Score 735; DB 2;
llarity 63.84; Pred. No. 1.9e-42;
Conservative 29; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC
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Best Local Simi.
Matches 139;
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N;Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Accession: 568241; 568214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
Submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrial A;Reference number: 568241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rat myeloma immunoglobulin kappa chain cDNA
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R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, PEBS Lett. 375, 273-276, 1995
A;Tille: Thermostable peroxidase activity with a recombinant antibody L chain-porphyri A;Reference number: S68211; MUID:96085223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Accession: 506084
A.Molecule type: mRNA
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A; Residues: 'NI', 3-212 <TAM>
A; Residues: 'NI' immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin
C; Keywords: immunoglobulin
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Pred. No. 1.8e-46;
7; Mismatches 52
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                                                                                                                                                                                                                                                                                                                                                                       R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3.
A;Reference number: S06084; MUID:90016888
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62.1%;
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Best Local Similarity
Matches 149; Conserv
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A; Residues: 1-218 <TAK>
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C;Superfamily: immunoglobulin.W region; immunoglobulin homology F;1-112/Domain: V region *status predicted <VRG>F;113-219/Domain: C region *status predicted <CRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12 $\frac{\pi_0^2}{25}$ A56169 Ig kappa chain V region (clone 23.2) - mouse (fragment)
                                                                                                                                                                                                                                  47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 SSTLTLSKADYEKHKVYAÇEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                 Ouery Match 57.68; Score 715.5; DB Best Local Similarity 60.38; Pred. No. 3.9e-41 Matches 132; Conservatives 39; Mismatches 4
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06-Jan-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grappa chain - sheep C; Species: Ovis orientalis ardes, Ovis ammon a C; Species: Ovis orientalis ardes, Ovis ammon c; Date: O6-Jan-1995 #sequence_revision O6-Jan-S, Accession S33161 F; Foley, R.C.; Beh, K.J. Submitted to the EMBL Data Library, July 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STLTLTKDEYERHNSYTCEATHYTSTSPI 209
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A;Nolecule type: mRNA
A;Residues: 1-210 <MON>
C;Superfamily: immunoglobulinry region; imm
C;Keywords: heterotetramer; immunoglobulin
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Matches 136;
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C; Species: Mus musculus (house mouse)
C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C; Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C; Accession: PC4203
R; Waws, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
Gene 173, 257-259, 1996
A; Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mc
A; Reference number: PC4203
A; Reference number: PC4203
A; Residues: I-219 < KWA>
A; Residues: I-219 < KWA>
A; Residues: I-219 < KWA>
A; Residues: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C; Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 Kappa chain precursor (15C5) - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: 514237
R; Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Bur. J. Blotchen. 192, 767-775, 1990
A; Thile: Construction and characterization of a recombinant murine monoclonal antibody (A; Reference number: S14236; MuID:91006173
A; Accession: S14237
A; Molecule type: MRNA
A; Residues: 1-234 cvAN>
A; Molecule type: MRNA
A; Residues: 1-234 cvAN>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin homology cIMM>
F; 36-110/Domain: immunoglobulin homology cIMM>
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                                                                                                                                                                 ESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKRTVAAPS 138
                                                                                                                                                                                                                                                                                                    VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 198
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57.1%; Pred. No. 3.3e-41;
iive 36; Mismatches 62.
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Matches 136; Conservative
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Rosenbaum, H.; God ï ö C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C;Accession: A56169
R;Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum J. Biol. Chem. 270, 6628-6638; 1995
A;Title: Recombinant antibodies in bloactive peptide design.
A;Reference number: A56169; More 195204454
A;Status: preliminary; not compared with conceptual translation
A;Status: mRNA (domestic sheep)
#text_change 20-Jun-2000 ÉSRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140 GVPPRESGSGSGTDFTLNÜHEVEEBDAATYYCQHSRELPWTFGGGTRLEIKRADAAPTVS 120 Gaps Gaps 9 SGIPDRFSGSGSGTDFTLFÆSRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKRTVAAPSV IFPPSDEQLKSGTASVVC#ENNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 1; ; 0 219; Length 210; Residues: 1-210 <mon> Length Indels

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Search completed: April 24, 2002, 15:11:36 Job time: 194 sec
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A; Description: Coordinate expression of antibody subunit genes yields high levels of fundal R: Reference number: $52028
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Description: Isolation and characterisation of sheep kappa light chain cDNA. Reference number: S33161
                                                                                                       A;Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;143-212/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                      TRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337 C.Superfamilly: immunoplobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;Keywords: heterotetramer; immunoglobulin F;16-95/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                     Length 230;
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                                                                                                                                                                                                                 57.4%; Score 713.5; DB 368.8%; Pred. No. 5.6e-41, iive 37; Mismatches 5.
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Best Local Similarity 60.7%
Matches 133; Conservative
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Matches 137; Conservative
                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-230 <FOL>
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A; Residues: 1-219 <VAN>
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                                  A; Accession: S33161
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C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C; Accession: S38865
R; Kipp, B.; Becker, W.; Schlaak, M.
Bubmitted to the EMBL Data Library, November 1993
A; Description: Combination of a defined specificity and desired isotype by cloning on A; Reference number: S38864
A; Reference number: S38865
A; Accession: S38865
A; Coss references: EMBL: Z27396; NID:q416538; PIDN:CAA81787.1; PID:q416539
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ption	homo sapien	homo sapien	homo sapien	mus musculu	mus musculu	homo sapien	mus musculu	mus musculu	mus musculu	mus musculu	homo sapien	homo sapien	mus musculu	homo sapien	homo sapien	mus musculu	homo sapien	homo sapien	homo sapien	homo sapien	mus musculu	homo sapien	homo sapien	homo sapien	homo sapien	mus musculu	mus musculu	mus musculu	homo sapien	homo sapien	mus m	wns w	homo sapien
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-!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER, 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND 83-LEU.
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01.NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III REGION HAH PRECURSOR.
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                              Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3 complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
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                                                             MEDLINE-69234734; PubMed-4893682
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InterPro; IPR003597; Ig_c1.
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Best Local Similarity 100.
Matches 106; Conservative
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SMART; SM00407; IGc1; 1.
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106 AA;
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P18135;
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Gaps
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MEDINE-88111307; Pubmed-3127527; Kipps T.J., Tomhave E., Chen P.P., Carson D.A.; Kipps T.J., Tomhave E., Chen P.P., Carson D.A.; Kipps T.J., Tomhave E., Chen P.P., Carson D.A.; Androantibody-associated kappen light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy."; J. Exp. Med. 167:840-852(1988).

-!- DISEASE THE PROTEINGIS ONE OF THE SURFACE IMMUNOGLOBULIN M AUTOANTIBODIES EXPRESED IN PATIENTS WITH CHRONIC LYMPHOCYTIC LEUKEMIA.
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MEDLINE-88171307; PubMed-3127527;
MEDLINE-88171307; PubMed-3127527;
MEDLINE-88171307; PubMed-3127527;
MEDLINE-88171307; PubMed-3127527;
Mattoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
-1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN MAUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC LEUKEMIA.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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COMPLEMENTARITY-DETERMINING
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01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-RAPPA CHAIN V-III REGION HIC PRECURSOR.
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FRAMEWORK
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PIR: PLO022; K3HUHA.
HSSP; P01789; 2MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_MC.
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SMART; SM00406; IGv; 1.
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118 TFGQGTKVEIKR 129
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HSSP; P01789; 2MCP.
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129 AA;
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P18136;
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KV3F_MOUSE
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McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-73140225; PubMed-4691517; McKean D.J., Potter M., Hood L.E.; Mouse inmunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burstein Y., Schechter I.; "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
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; Pred. No. 8.5e-37;
11; Mismatches 16; Indels 3
                                                                                                                                    IG KAPPA CHAIN V-III REGION HIC.
PRAMENOKK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
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COMPLEMENTARITY-DETERMINING
JK1 SEGMENT.
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Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
PIR; A01935; KVMSM6.
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR
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                                           Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Best Local Similarity 77.38
Matches 102; Conservative
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118 TFGQGTKVEIKR 129
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Mammalia; Eutheria;
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KV3I_MOUSE
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BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT PREPRIED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
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MEDLINE-73140224; PubMed-4120629;
MECKEAN D. J., POtter M., Hood L.E.;
"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-37.
MEDLINE=7825887; PubMed=98179;
MEDLINE=7825887; PubMed=98179;
Burstein Y., Schechter Y.;
Primary structures of Niterminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: inplications on the organization and controlled expression of immunoglobulin genes.";
Biochemistry 17:2392-2400(1978).
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Mammalia; Eutheria; Rodėntia; Sciurognathi; Muridae; Murinae; Mus
                                                                                     IG KAPPA CHAIN V-III REGION MOPC 63.
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                                                                                                   FRAMEWORK 1. COMPLEMENTARITY-DETERMINING 1.
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                                                                                                                                                                                                                                                                                                    Length 131;
                                                                                                                                     FRAMEWORK 2. COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                   16; Indels
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                                                                                                                                                                                                                                                                                                 42.0%; Score 522; DB 1; 74.8%; Pred. No. 1.2e-36; Ive. 17; Mismatches 16
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BY SIMILARITY
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Pfam: PF00047; 19; 1. Pfam: PF00047; 19; 1. Pfam: PF000405; 1Gv: 1. Ffamunoglobulin V region; Signal.
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InterPro; IPR003596; Ig_W.
Pfam; PF00047; ig; 1.
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121 TFGGGTKLEIK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                    ô
                                                                                                                                                                                                                                          61 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPR 120
                                                                                                                                                                   0; Gaps
                                                                                                                                                                                     1 METDTILLMVLLLMVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                 IG KAPPA CHAIN V-III REGION IARC/BL41.
        IG KAPPA CHAIN V-III REGION MOPC 321.
FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-86041852; PubMed-2997711;
Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulin kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3.
                                                                                                                                              Length 132;
                                                                                                                                             ch 40.9%; Score 508; DB 1; Length 13;
1 Similarity 67.4%; Pred. No. 1.7e-35;
89; Conservative 26; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY - DETERMINING FRAMEWORK 3.
                                                   COMPLEMENTARITY - DETERMINING
                                                                                                               9F3B809BB773FBE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                              128 AA
                                                                                            BY SIMILARITY.
                                         FRAMEWORK 2
                                                                                  FRAMEWORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 13:6499-6513(1985).
                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin V region; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A01899; K3H441.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR0013596; Ig_V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                               14523 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z00021; CAA77316.1; -.
                                                                                                                                                                                                                                                                                                                                             STANDARD;
20
132
43
43
58
73
80
112
1112
132
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128
43
54
59
76
108
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121 TFGSGTKLEIKR 132
                                                                                                                                                                                                                                                                      121 TFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                          43
132
132 AA;
                                                                                                                                           Query Match
Best Local Similarity
Matches 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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21
44
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70
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                                                                                DOMAIN
DISULFID
NON_TER
SEQUENCE
                                       DOMAIN
DOMAIN
DOMAIN
          CHAIN
                                                                     DOMAIN
                              DOMAIN
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KV3K_HUMAN
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                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                1 METDTILLMVLLLMVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-79073152; PubMed=103003; Weigert M., Gatmaitan Low Lon E., Schilling J., Hood L.E.; Weigert M., Gatmaitan Low Lon E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin diversity."

Nature 276:785-790(1979)
                                                                                                                                       4 ;
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0
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 COMPLEMENTARITY - DETERMINING 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
COMPLEMENTARITY-DETERMINING 2.
COMPLEMENTARITY-DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 473; DB 1; Length 111;
Pred. No. 1.1e-32;
8; Mismatches 13; Indels
                                                                                                       Length 128;
                                                                                                                                      19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK 3. COMPLEMENTARITY-DETERMINING
                                                            CC8957F0FE3B9012 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12002 MW; 7A5FCB586C306D29 CRC64;
                                                                                                  38.8%; Score 482; DB 1;
73.5%; Pred. No. 2.3e-33;
tive. 12; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11G Kappa CHAIN V-III REGION PC 7043.
                                                                                                                                                                                                                                                                                                                                                                                            111 AA.
                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK 4.
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse). Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                            140%0 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.1%;
81.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A01937; KVMS43.
InterPro: IPR003006; IgHHC.
InterPro: IPR003596; IgH-V.
Prfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                     Query Match
Best Local Similarity 73.59
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
 117
128
108
128
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60333
                                                                                                                                                                                                                                                                                                       117 TFGQGTKLEIKR 128
                                                                                                                                                                                                                                                                                      121 TFGQGTRLEIKR 132
109
118
43
128
128 AA;
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39
54
61
01
23
111
111 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 90;
                                                                                                                                                                                                                                                                                                                                                                                            KV3M_MOUSE
DOMAIN
DOMAIN
DISULFID
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NON_TER
SEQUENCE
                                            NON_TER
SEQUENCE
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DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                              RESULT 7
KV3M_MOUSE
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Gaps

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14; Indels

Length 111;

80

9

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1 DIVLIQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYTASNLES
                                                                                                                                                                                                                                                                                                                                                        21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                 81 GIPDRESGSGSGTDFTLTISRLEPADFAVYYCOOSNEDPRTFGGGTRLEIK 131
                                                                                             FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2.
                                                                              COMPLEMENTARITY - DETERMINING 1.
                                                                                                                                                COMPLEMENTARITY - DETERMINING 3.
                                                                                                                                                                                                                          7A4ADE4D6C256D29 CRC64;
                                                                                                                                                                                                                                                                              37.8%; Score 469; DB 1;
ilarity 80.2%; Pred. No. 2.3e-32;
Conservative 8; Mismatches 14;
                                                                                                                                                                     FRAMEWORK 4.
BY SIMILARITY.
                                                         FRAMEWORK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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MEDLINE-79073152; PubMed-103003;
                                                                                                                                                                                                                          MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; E01937; KVMS69.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-V.
Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region-
DOMAIN 24 38

DOMAIN 39 53

DOMAIN 64 60

DOMAIN 61 92

DOMAIN 102

DOMAIN 102

DOMAIN 102

DOMAIN 102

DOWAIN 102

DOWAIN 102

NON_TER 111
                                                                                                                                                                                                                          12071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diversity.";
Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
388
53
60
101
111
111
                                                                                                                                                                                                                          111 AA;
                                                                                                                                                                                                                                                                                                 Local Similarity
nes 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KV3Q_MOUSE
ID KV3Q_MOUSE
AC P01669;
                                                                                                                                                                                                         NON_TER
SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                    Query Match
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Matches
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                          MEDLINE-79073152; PubMed-103003; Welgert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY - DETERMINING 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.9%; Score 471; DB 1; Length 11
80.2%; Pred. No. 1.6e-32;
Live 9; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11952 MW; 2058BB50CE306D31 CRC64;
                                                                                                        21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 7183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                           111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK 4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IG KAPPA CHAIN V-III REGION PC 6308.
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=79073152; PubMed=103003;
                                                                                             01, Created)
                                                                                                                                                                                                                                                                                                                                                                    PIR; B01937; KVMS83.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unature 276:785-790(1978).
Nature 276:785-790(1978).
PIR; C01937; KVMSO8.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
                                                                                                                                                                                                                                                                                                                                     diversity.";
Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89; Conservative
                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
38
53
60
60
101
111
                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                             (Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                         21-JUL-1986 (
21-JUL-1986 (
15-JUL-1999 (
                                                         KV3N_MOUSE
P01666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KV30_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
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SEQUENCE
                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
KV30_MOUSE
DE MOUSE
DT 21-JUL.
DT 21-JUL.
DT 15-JUL.
DE IG KAPIO
OC MAMMAL.
OC MAMMAL.
OC MARMAL.
OC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                    RESULT 8
KV3N_MOUSE
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Gaps
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Musculus (Mouse). %
Mukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weigert M., Gatmaitan L. Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
37(5%; Score 466; DB 1; Length 111; 79§3%; Pred. No. 4e-32; Live 10; Mismatches 13; Indels
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COMPLEMENTARITY-DETERMINING 3.
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                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KADAR CHAIN V-III REGION PC 7769.
                                                                                                                                             111 AA
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BY SIMILARITY
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KV3B_HUMAN
P01620;
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P01664;
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SEQUENCE
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                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDIAGE 3083417; MEDLINE-8617570; PubMed-3083417; Jirlk F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P., Goldfien R., Carson D.A.; "Cloning and sequence determination of a human rheumatoid factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Gaps
                                                                                               20-MĀR-1987 (Rel. 04, Created)
1-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last amondation update)
16 KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).
16 KAPPA CHAIN V-III REGION CLL PRECURSOR (RHEUMATOID FACTOR).
17 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIK 131
            IG KAPPA CHAIN V-III REGION CLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5C13B411BE60CC14 CRC64;
                                                                                                                                                                                                                                                         light-chain gene.";
Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
                                                                            129 AA
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BY SIMILARITY.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
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129
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129
129 AA;
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                                                                           KV3H_HUMAN
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SEQUENCE
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Andrews D.W., Capra J.D.; "Amino acid sequence of the variable regions of light chains from two idlotypically cross-reactive human IgM anti-gamma-globulins of the Wa
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"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions."

Proc. Antl. Acad. Sci. U.S.A. 75:3913-3917(1978).

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.0%; Score 459.5; DB 1; Length 109; 79.5%; Pred. No. 1.4e-31; 1ve 10; Mismatches 10; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;
                                                      (Rel. 01, Last sequence update) (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 ARPPA GHAIN V-III REGION CBPC 101.
AA.
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109
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                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seque
15-JUL-1999 (Rel. 38, Last annot
IG KAPPA CHAIN V-III REGION SIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
MEDLINE=79012520; PubMed=99744;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003566; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 79.58
Matches 89; Conservative
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
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RESULT 15
KV3E_HUMAN
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MEDLINE=72188439; PubMed=5027703;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Interesting the structure. The primary structure of a monoclonal immunoglobulin L-chain of Kappa-type, subgroup 3 (Bence-Jones protein T1). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

-: MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                               21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GIPARFSGSGSGIDFTLNIHPVEEDAATYYCQQSNEDPYFFGGGTKLEIK 111
                           COMPLEMENTARITY-DETERMINING 1. FRAMEWORK 2.
                                                                                                                                                                                                                                                                         Score 458; DB 1; Length 111;
Pred. No. 1.8e-31;
                                                                                             FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING
                                                                        COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                         14; Indels
                                                                                                                                                                                                          E2B1AD98AD965962 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 AA
                                                                                                                                                              BY SIMILARITY.
                                                                                                                                         FRAMEWORK
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                                                                                                                                                                                                          MW;
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21-JUL-1986 (Rel. 01, Last seq
                                                                                                                                                                                                                                                                           36.9%;
78.4%;
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InterPro; IPR003596; Ig_v.
Pfam; PF0047; ig; 1.
SMART; SM00406; IGV; 1.
23
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11964 1
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Best Local Similarity 78.49
Matches 87; Conservative
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HSSP; P01789; 2MCP.
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P01622;
                                                                                                                                    DOMAIN
DISULFID
NON_TER
SEQUENCE
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                                                                     DOMAIN
DOMAIN
DOMAIN
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KV3D_HUMAN

ID RV3D_HUMAN

AC P01622

DT 21-JUL

DT 21-JUL

DT 15-JUL

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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
PIR, A01896, YASUWL.
INTERPRO; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains from t didtypically cross-reactive human IgM anti-gamma-globulins of the
                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 109;
                                                                                                       Homo sapiens (Human). **
Homo sapiens (Human). **
Bukaryota; Metazoa; Chozdata; Craniata; Vertebrata; Eutele
Mammalla; Butherla; Primates; Catarrhinl; Hominidae; Homo
NCRT TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 452.5; DB Pred. No. 5.2e-31
                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 ARPPA CHAIN V-III REGION WOL.
HOMO Sapiens (Human).
109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                  MEDLINE=82046598; PubMed=6794615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11746 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 7935
watches 89, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin V region
STANDARD
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109
109 AA;
KV3E_HUMAN
P01623;
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NON_TER
SEQUENCE
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Search completed: April 24, 2002, 15:13:45 Job time: 322 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:08:22; Search time 86.76 Seconds

(without alignments)
401.254 Million cell updates/sec

Title: US-09-499-662-50

Perfect score: 1242
Sequence: 1242
Sequence: 1 METDTILLWVLLLWVDGSTG......EVTHQGLSSPVTKSFNRGEC 238
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_nwertebrate:*
sp_mammal:*

SPTREMBL_17:*

Database :

sp_organelle:* sp_phage:*

4.55: 66: 77: 10: 111: 113:

sp_plant:*

Result Cuery No. Score Match Length DB ID 2 686 55.2 214 11 099M37 2 686 55.2 214 11 099M37 3 445.5 35.9 109 4 09UL78 6 405 32.6 108 4 09UL78 7 394 31.7 108 4 09UL77 9 385.5 31.0 109 4 09UL83 9 31.3 108 4 09UL77 9 385.5 31.0 109 4 09UL80 11 375.5 30.2 107 4 09UL81 12 363 29.2 103 11 099M10 13 35.2 29.1 114 4 09UL80 14 345.5 27.8 106 5 09UL80 15 330 26.6 99 11 09UL70 099J18 mus musculu 09J18 homo sapien 09UL80 09UL80 mus musculu 09UL80 09UL80 09UL80 09UL80 09UL80 09UL80 09UL80 09UL80 09UL80 09UL80 09UL80 00UL80 09UL80 00UL80 00

1;

126

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Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                            35.9%; Score 445.5; DB 4; 78%6%; Pred. No. 6e-34; 11vg. 7; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                              109
                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                        EMBL; AF035036; AAD56272.1; --
HSSP; P01789; 1MCP.
InterPro; IPPR003306; 1ggMrC.
InterPro; IPPR003396; 1ggWr.
Pfam; PF00047; 19; 1. 3
SMART; SM0406; IGV; 1. 3
NON_TER 1 1
NON_TER 109 109
SEQUENCE 109 AA; 11646 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 AA; 11928 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 34.0%;
Best Local Similarity 75.0%;
Matches 84; Conservative
                                                                                                                                                                                                       Local Similarity 78%
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                  DOMAIN
                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Matches
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                                                                                                                                                                 Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09UL78
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN FREACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
HOMO SAPIENS (HUMAN).
EURARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 55.2%; Score 686; DB 11; Length 214; Best Local Similarity 58.7%; Pred. No. 7e-56; Matches 128; Conservative 34; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                         52BA205FDE995E2A CRC64;
                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
XAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                   EMBL; AF152371; AAD40242.1; -. HSSP; P01789; 1MCP.
InterPro; 1PR003600; 1g_11ke.
InterPro; 1PR003596; 1g_MtC.
InterPro; IPR003596; 1g_M.
                                                                                                                                                                                                                                                                                                                                                                              214 214
214 AA; 23922 MW;
                         PRELIMINARY;
                                                                                             Mus musculus (Mouse)
                                                                                                                                               [1]
SEQUENCE FROM N.A.
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                                                                                                                                  NCBI_TaxID=10090;
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NON_TER
SEQUENCE
                      Q9R1A5
Q9R1A5;
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fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOCLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MY-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 GIPDRESGSGSGTDFTLTGSRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIKR 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 422.5; DB 4; Length 109;
Pred. No. 8.2e-32;
8; Mismatches 17; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                  Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDAG-9614934; MED. N. MED. N. MED. N. MED. Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243325F72C7DAC83 CRC64;
                                                                                                                                                                                                                                                                                                        109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;
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11738 MW; C06681716C4D16F3 CRC64;

108 AA;

3

Page

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SEQUENCE
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01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 APRLLIYAASNLESGIPDRFSGS--GSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 GTRLEI-KRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 QESVTEQDSK--DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.8%; Score 419.5; DB 11; Length 235; ilarity 42.2%; Pred. No. 4.1e-31; Conservative 36; Mismatches 88; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                    Strausberg R.; Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC002129; AAH02129.1; -. SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;
                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                  235 AA.
                                                                                  PRT;
                                                                                                                                                                                              UNKNOWN (PROTEIN FOR MGC:6743).
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HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                   Mus musculus (Mouse)
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Best Local Similarity
Matches 100; Conserv
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Q9UL79;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                           01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-JUA 2001 (TrEMBLrel. 17, Last annotation update)
01-JUA EACTIVE IMMUNGIOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                              Gaps
                                                                                        21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
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                                                                                                               1 DIQMIQSPSSLSASVGDRVIIICRASQSI----SSYLNWYQQKPGKAPNLLIYAASSLQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                81 GIPDRFSGSGSGTDFTLTTSRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKR 132
                                                                                                                                                                                                   81 GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKR 132
Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 108;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98277139; Pubmed-9614934; Ralis N.N., Berney Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9F9C5A92EBA96EEA CRC64;
                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
32.6%; Score 405; DB 4; 67.9%; Pred. No. 3.4e-30; ive 16; Mismatches 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31#7%; Score 394; DB 4;
70.5%; Pred. No. 3.5e-29;
14vg. 11; Mismatches 18
                                                                                                                                                                                                                                                                                                                                          ¥.
                                                                                                                                                                                                                                                                                                                                        108
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                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF035031; AAD5626#1; -. HSSP; P01607; IRET. InterPro; IPR003006; IQ_MRC. InterPro; IPR003596; IQ_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 108 °
108 AA; 11834 MW;
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                                            76; Conservative
                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; 19; 1. SMART; SM00406; IGv; 1.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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SEQUENCE
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                                              Matches
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81 GIPDRFSGSGSGTDFTLTESRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKR 132

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                                                                                                                                                                                                                                                                                    1;
                                                                            fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clin. Immunol. Immunopathol. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                      21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES
                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                 Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                81 GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKR 132
                                MEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                           4; Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 31.2%; Score 387; DB 4; Length 108; Best Local Similarity 64.3%; Pred. No. 1.6e-28; Matches 72; Conservative 16; Mismatches 20; Indels
                                                                                                                                                                                                                                                         31.3%; Score 389; DB 4; Length 10 67.0%; Pred. No. 1e-28; ive 12; Mismatches 21; Indels
                                                                                                                                                                                                            108 108
108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF035044; AAD56280.1; -. HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                        EMBL; AF035035; AAD56271.1; -. HSSP; P01607; 1REI. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Ffam; PF00047; Ig; 1. SWART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11633 MW;
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 67.0°
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AA;
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NON_TER
SEQUENCE
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Young D.C.
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fetus.";
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                                                                                           Clin.
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Q9UL70
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fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13. Created)
01-MAY-2000 (TrEMBLrel. 13. Last sequence update)
01-MAY-2001 (TrEMBLrel. 17. Last annotation update)
01-JUN-2001 (TrEMBLrel. 17. Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                            Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosun-reactive autoantibodies in rheumatic carditis and normal
fetus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.0%; Score 385.5; DB 4; Length 109; 69.0%; Pred. No. 2.2e-28; ivg 12; Mismatches 18; Indels 5
                                                                                                                                                                                                                                                                                                           Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                        Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA.
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                                                                                              PRT;
                                                                                                                                                                                                                                                                                             MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF035029; AAD56265.1; --
HSSP; P01607; IREI.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; Ig; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human). **
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 69.00
                                                                                              PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 AA;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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Q9UL81;
                                                                                              Q9UL85
                                                           RESULT 10
Q9UL85
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Gaps

21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80

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NON_TER NON_TER SEQUENCE

Query Match

Matches

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Song X.T., Feng Z.O., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.,
"Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
Schistosoma japonicum "A.
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                        01-MAY-2000 (TremBirel 131, Created)
01-MAY-2000 (TremBirel 131, Last sequence update)
01-UNY-2001 (TremBirel 17, Last annotation update)
MYOSIN-FRACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 DIVLTQSPGTLSLSPGERATLSCKASQSVDY-DGDSYMNWYQQKPGQAPRLLIYAASNLE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
                                                                                                                    Homo sapiens (Human). अ
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                          'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 SGIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNE-DPRTFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

BEDLINE-90277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.1%; Score 362; DB 4; Length 11 60,5%; Pred. No. 3.5e-26; Live 21; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 12775 MW; 070E31E210D1CB01 CRC64;
      114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF207620, AAF19434.1; --
HSSP, P01679; 2FBJ,
InterPro; IPR003006; IQ_MHC.
InterPro; IPR003586; IQ_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV, 1.
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF035034, AAD56270.1; -. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Iggv. Pfam; PF00047; ig; 1. SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIABLE REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
  PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                fetus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
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Q9U410
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        Op
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Malkiel S., Liao L., Cunningham M.W., Diamond B.;
"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                  21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                      30 TLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLESGIPDRFSGS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                2;
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0
                                                                                                                                                                                                                                                                    ^ Match 30.2%; Score 375.5; DB 4; Length 107; Local Similarity 64.3%; Pred. No. 1.8e-27; les 72; Conservative 18; Mismatches 17; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                           81 GIPDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.2%; Score 363; DB 11; Length 103; ilarity 66.7%; Pred. No. 2.5e-26; Conservative 17; Mismatches 17; Indels
                                                                                                                                                                                                                107 AA; 11501 MW; 070549FDE0754748 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 103
103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 GSGTDFTLTISRLEPADFAVYYCQOSNEDPRTFGQGTRLEIK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF206026, AAF69324.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam: PF00047; ig; 1.
SMART: SMO0406; IGV; 1.
NON TER.
                                                  EMBL, AD56269.1; -. HSSP; P80362; 1WTL. InterPro; IPR003006; Ig_MHC. InterPro; IPR003506; Ig_V. Pfam; PF00047; 49; 1. SWART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                              107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                107
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STRAIN-BALB/C; TISSUE-SPLEEN;
shinobara N., Demura T., Fukuda H.;
"Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction method.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            method.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                   Gaps
                                                                                                                            23 VLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLESGI 82
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                                                                                                                                                Query Match 26.7%; Score 331; DB 11; Length 298; Best Local Similarity 46.1%; Pred. No. 8.9e-23; Matches 70; Conservative 20; Mismatches 40; Indels 22; Gaps
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                                                                                                                                                                                                                                                                                                                     090YF0;

01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

CN 8 SCFV.

CN 8.

Mus musculus (Mouse).

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musculus;
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                                                                    Length 106;
                                                                                                                                                                                          83 PDRFSGSGSGTDFTLTISRLEPADFAVYYCQQSNEDPRTFGQGTRLEIK 131
                                                                                                                                                                                                              Query Match 27.8%; Score 345.5; DB 5; Length Best Local Similarity 61.5%; Pred. No. 1.1e-24; Matches 67; Conservative 13; Mismatches 24; Indels
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-SPLEEN;
Shinohara N., Demura T., Fukuda H.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
106
11478 MW; F20F544426BAE63E CRC64;
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HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; PR003596; Ig_V.
Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv; 2.
SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
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1 METDTILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. **Since ## Annual ## Annua

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Description	Anti-Fas humanised	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Anti-Fas humanised	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas
SUMMARIES	AAW83032	AAB14773	AAW90923	AAW83035	AAB14778	AAW90928	AAW83033	AAB14774	AAW90924	AAW83031	AAB14772
DB	19	21	21	19	21	21	19	21	21	19	21
% Query Match Length DB	238										
% Query Match	100.0	100.0	100.0	99.4	99.4	99.4	99.4	99.4	99.4	96.5	96.5
Score	1246	1246	1246	1239	1239	1239	1238	1238	1238	1202	1202
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21..131 /label= Variable 132..238 /label= Constant

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AAW90922 Humanised anti-Fas AAB1477 Humanised anti-Fas AAW90927 Humanised anti-Fas AAW90933 Humanised anti-Fas AAW90930 Humanised anti-Fas AAW90930 Humanised anti-Fas AAW93702 The Kappa chain of AAX93729 The Kappa chain of AAX93729 Humanised anti-L-s AAX93729 Human bone marrow-Human bone marrow-Human bone marrow-Human reshaped F19 AAX95061 Mus musculus anti-AAX9508 AAX9378 Full variable ligh AAX9378 Full variable ligh	AAV93733 The kappa chain of AAV93704 AAV93704 The kappa chain of AAV93731 The kappa chain of AAV33312 The kappa chain of AAV33312 The kappa chain of The kappa chain of AAV33312 The Muman sed MaEll Vernaman and the center of AAV14461 Human movel protein Human novel protein Human novel protein AAV14464 Human novel protein AAV14464 Human novel protein AAV5030 Human novel protein AAV50604 Mus musculus anti-AAW95660 AAW95660 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-AAW95664 Mus musculus anti-	ALIGNMENTS 238 AA. HFE7A light chain HM type.	HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogens syndrome; pernicious anaemia, Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.	/Qualifiers S1g_peptide Mat_protein
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	20000000000000000000000000000000000000	RESULT AAW83032 ID AAW XX AC AAW XX XX DY DE ANT		XX

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Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, Theumatoid arthritis, autoimmune haemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arterfosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAW83042) entailed making P47A and K49R amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell E. coli pHSGHM17 SANK 73597 harbors plasmid pHSGHM17 carrying a fusion fragment of the humanised Hw type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6072 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native expressing Fas, and of inhibiting Fas:induced apoptosis in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the HM type humanised light
                                                                                                                                                                                                                                                                                                                                                                                   Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 200; 292pp; English
                                                74..80
/label= CDR_L2
/note= "claim 9"
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/label= CDR_L1
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97JP-0169088.
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O, Nobufusa
                                                                                                                                                                                                                                                                                                                                                 (SANY ) SANKYO CO LTD
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Length 238; 0; Indels 100.0%; Score 1246; DB 19; 100.0%; Pred. No. 6.2e-67; 0; Mismatches 238; Conservative Query Match Best Local Similarity Matches

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1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY

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61 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120

The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas, suntibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFF7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFF7A, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, attendedselves, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft@rejection; light chain. Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains TFGQGTRLEIKRTVAAPSWFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180 181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; Humanised anti-Fas antibody light chain, SEQ ID NO:52. Claim 20; Page 80-81; 139pp; Japanese. AAB14773 standard; Protein; 238 AA 98JP-0276883. 99JP-0278301 24-NOV-2000 (first entry) Chimeric - Mus musculus, Chimeric - Homo sapiens. (SANY) SANKYO CO LTD. WPI; 2000-485645/43. N-PSDB; AAA72125. anti-Fas antibody JP2000169393-A. 30-SEP-1999; 30-SEP-1998; 20-JUN-2000. antibodies. AAB14773; 121 g οχ ŏ g q

ö Gaps ö Length 238; Indels DB 21; ö 100.0%; Score 1246; DB 21 100.0%; Pred. No. 6.2e-67; 1ve 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 238; Conservative 238 AA; Sequence

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Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotrophc; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashlmoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosuparessive, thyronimetic, antirheumatic, nephrotropic, antilhertillty, neuroprotective, antiatreniosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                        QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                              121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                    metdtillwv111wvpgstgdiv1tqspgtls1spgerat1sckasqsvdydgdsymnwy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example reference 14; Page 117-118; 263pp; English.
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                                                                                                                                                                                                                                                                                                                                                    AAW90923 standard; Protein; 238 AA
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98JP-0276882.
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N-PSDB; AAA11563
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30-SEP-1998;
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inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic nemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Pas antibody HEPZA light chain HM type which is used in the method described in the invention.
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100.0%; Pred. No. 6.2e-67
:ive 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.
                                                                                                                                                                                                                                                                                                                                                        238 AA;
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Matches 238;
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Region

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This is the amino acid sequence of the PDHM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAM83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host cell Escherichia coll pHSM2 SANK 70198 harbors plasmid pHSHM2 carrying a fusion of the humanised pDHM type HFF7A light chain and deposited as FERM BP-672 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFF7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal models. Treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune graft press and also to treat such diseases, including autoimmune graft press and sot diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune graft press and such account of the provise such and also to treat such diseases, including autoimmune graft press and passes and provises ansemia, addisease and addisease Sigutems Condense Pressions ansemia, addisease and passes and provises and passes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            οκο r, Jun O, Kimihisa I;
Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; Page 220-221; 292pp; English.
                                                                                             /nouc
74..80
/label= CDR_L2
..to= "claim 9"
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'label- Constant
   /label= Variable
                                                                                                                                                                                     /label= CDR_L3
/note= "claim 9"
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                                                       44..58
/label= CDR_L1
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97JP-0082953.
97JP-0169088.
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N-PSDB; AAV70078.
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25-JUN-1997;
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                    Region
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                                                                                                              Region
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Gaps ; 0 99.4%; Score 1239; DB 19; Length 238; 99.2%; Pred. No. 1.6e-66; 1ive 2; Mismatches 0; Indels 0 Best Local Similarity 99.2 Matches 236; Conservative Query Match

1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60

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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas, or a bumanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerois, myocarditis, cardiomyopathy, allergy, atopy, arteriosclerois, myocarditis, cardiomyopathy, allergy, atopy arteriosclerois, myocarditis, cardiomyopathy, and organ graft rejection. Sequences AAB14772-B14774 and ABB14777-B14778 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                          murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
                               TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                    1 metdtillwvlllwvpgstgeivltgspgtlslspgeratlsckasgsvdydgdsymnwy 60
                                                                                                                                                                  Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
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                                                                                                                                                                                                                                                                                      AAB14778 standard; Protein; 238 AA
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Chimeric - Homo sapiens.
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238 AA;

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                                                                                                                                                                                                                                                                                                                                                                    Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; antiallergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New humanized anti-Fas antibody, useful for treating or preventing e.g.
                                                                                                        QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCOOSNEDPR 120
                                                                                                                                          TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                            1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
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                                                                                                                                                                                       GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                       Indels
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Pred. No. 1.6e-66;
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                                                                                                                                                                                                                                                                                                                                              Humanised HFE7A designed light chain protein #2.
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        99.28;
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98JP-0276882.
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                      Matches 236; Conservative
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           Best Local Similarity
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antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
composits by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
diseases associated with the Fas/Fas ligand system, especially systemic
complete supplementations, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anenia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, alleray, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
completes an alcoholic), and transplant rejection. (I) selectively
cinhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
cells. They bind to both human and murine Fas, so can be evaluated in
complete and induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
the native ligand, do not induce liver disease, and have reduced risk of
the native manised anti-murine antibody response. This sequence represents
the nearbook and the factor of the active site of fas, is a con the contractive in the active of a humanised anti-murine antibody response. This sequence represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic luque erythematosus; graft versus host disease; sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; atteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
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Pred. No. 1.6e-66;
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/label= Sig_peptide
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Best Local Similarity
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to evaluate drugs in animal models and to treat Fas-associated uses e.g. autoimmune disease, allergy, atopy, arteriosclerosis.
                                                                                                                                                                                                                                          New antibodies and proteins bind conserved epitope of Fas antigen
                                                                                                                                                                                                Jun O, Kimihisa I;
, Tohru T;
       label = Mat_protein
                                                                                                                                                                                                                                                                           Claim 21; Page 202; 292pp; English.
                                                                                                                                                                                                Hiroko Y, Ju
1 S, Shin Y,
                                                                                 113..121
/label= CDR_L3
/note= "claim 9"
                    'label- Variable
                           /label= Constant
                                                     /note= "claim 9"
74..80
                                                                            /note= "claim 9"
                                                                                                                                                                                                                                                               myocarditis, hepatitis and AIDS
                                                /label= CDR_L1
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                                                                                                                                                                                                       Masahiko O, Nobufusa
                                                                                                                                                                                                Hideyuki H,
                                                                                                                                                                                                                    WPI; 1998-543440/47.
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This is the amino acid sequence of the MM type humanised light

C chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli

SANK 73697 hatboors plasmid pH8CMM6 carryling a fluation fragment of the

C humanised MM type HFE7A light chain and DNA encoding the region of

human kappa chain, and is deposited as FERM BP-6071 (claimed). The

culturing host cells. Humanised versions of HFE7A (see AAM83031-37),

like native HFE7A, are capable of inducing apoptosis in abnormal

c cells expressing Fas, and of inhibiting Fas-induced apoptosis in

normal cells. The humanised antibodies are used to evaluate, in

calls expressing Fas, and of inhibiting Fas-induced apoptosis in

calls expressing to treat such diseases, including autoimmune

interactions, and also to treat such diseases, including autoimmune

c disease (e.g. systemic lupus erythematosus, Hashimoto's disease,

c datases (e.g. systemic lupus erythematosus, Hashimoto's disease,

disease, rheumatoid arthritis, autoimmune hemolytic anaemia,

disease, rheumatoid arthritis, autoimmune hemolytic anaemia,

disease, rheumatoid arthritis, autoimmune hemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular neephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).

Gaps METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60 ö Indels Score 1238; DB 19; Pred. No. 1.8e-66; 1; Mismatches 1; 99.4%; Conservative Ouery Match Best Local Similarity Matches 236, Conserv

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Length 238;

Score 1238; DB 21; Pred. No. 1.8e-66;

99.48;

Query Match Best Local Similarity

238 AA;

Sequence

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Length 238;

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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas.antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a bumanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA, via its interaction with Fas, the antibody of the invention acts as a medulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allery, atopy, arteriosclerois, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                 Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand, apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft_rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand aystem e.g. autoimmune diseases, contains
                  TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                  QOKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                   GNSQESVTEQDSKDSTYŞLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                   Humanised anti-Fas antibody light chain, SEQ ID NO:54.
                                                                                                                                                                                                                                                            AAB14774 standard; Protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 83; 139pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Mus musculus.
Chimeric - Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; antiallergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyrominetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; basedow's disease; trombopenia purpura; allergy; insulin dependent diabetes mallitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotrople, antilnfertility, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
                                                                                                                      QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                                                    TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                              0; Gaps
                                                                                                                                                                                                                                      181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                            Humanised anti-Fas antibody HFE7A light chain MM type protein.
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 Indels
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 Mismatches
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98JP-0276882.
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Conservative
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Matches 236;
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ID AAW9
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apptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic curves a sociated with the Fas/Fas ligand system, especially systemic curves us to state and the system of spaces. However, graft versus host disease, Slorgen's syndrome, pernicious or hypoplastic canemia, Addison's disease, soleroderma, Goodpasture syndrome, Crohn's disease, autcimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabbetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively cells, they bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody HFEPA light chain MM type which is used in the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 qqkpgqppklliyaasnlesgipdrfsgsgsgtdftltihpveeedaatyycqqsnedpr 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
cardiant and hepatropic activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1238; DB 21
Pred. No. 1.8e-66;
1; Mismatches 1
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/label= Sig_peptide
21..238
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chain of murine anti-human Fass monoclonal antibody HFEFA.

CHumanisation of the murine sequence (see AAM83042) entailed making P47A, K49R, H80S, P81R, V82L, E85A, A87F and T89V amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli pHSGHH7 SANK 73497 harbors plasmid pHSGHH7 carrying a fusion fragment of the humanised HH Type HFEFA light chain and DNA encoding the region of human colimmunoglobulin kappa chain, and is deposited as FERM BP-6073 (claimed). The inventron provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFEFA (see AAW83031-37), like native HFEFA, are capable of inducing capptosis in abnormal cells expressing Fas, and of inhibiting Fas-Induced apoptosis in normal cells. The humanised antibodies considered to evaluate, in animal models, treatments of diseases that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sjogren syndrome, pernicious anamia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thromopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of the HH type humanised light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 199-199; 292pp; English.
 'label= Mat_protein
                                                                                                                                     74..80
/label= CDR_L2
/note= "claim 9"
              11..131
|Tabel= Variable
                                                                                     /label= CDR_L1
/note= "claim 9"
                                                   32..238
'label= Constant
                                                                                                                                                                                                                              /note= "claim 9"
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97JP-0169088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (SANY ) SANKYO CO LTD.
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N-PSDB; AAV70074.
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                                                                                                                                                                                                                                                                                                                                      30-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            25-JUN-1997;
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                                                                                                                                                                                                                                                                 AU9859701-A.
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas Fantibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFETA, or a humanised version of HFETA containing identical CDRs (complementarity determining regions) to antibody HFETA. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                allergy, acopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFD7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Fas antibody; monoclonal antibody HFB7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; appoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft@rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand gystem e.g. autoimmune diseases, contains anti-Fas antibody - \frac{\pi}{4\pi}
                                                                      61 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                         121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                    9
                                                                                                                                                                                                                       181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                      1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Humanised anti-Fas antibody light chain, SEQ ID NO:50.
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                                                                                                                                                                                                                                                                                                                                                   AAB14772 standard; Protein; 238 AA
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Chimeric - Homo sapiens.
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238 AA;

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Gaps

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Length 238; Indels

Query Match 96.5%; Score 1202; DB 19; Best Local Similarity 97.1%; Pred. No. 2.5e-64; Matches 231; Conservative 1; Mismatches 6;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory,
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                                                                                                                                                                                                                           121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                    61 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                     Gaps
                                                                   1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                    181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Humanised anti-Fas antibody HFE7A light chain HH type protein.
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     Length 238;
                                     Indels
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Score 1202; DB 21
Pred. No. 2.5e-64;
1; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                            AAW90922 standard; Protein; 238 AA.
 96.5%;
97.1%;
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                                   Conservative
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                 Similarity
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                     Best Local Sim
Matches 231;
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Best Local S
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(B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised antibody HFE7A light chain HH type which is used in the method described in the invention.
                                                                                                                                                                                                                                                                                               viral
                  immunomodulatory, dermatological, immunosuppressive, thyromimetic, antithemmatic nephrotropic, antiinfartility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, heumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomeriliosphritis, hepatitis (fulminant, chronic, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1\ \texttt{metdtillwvlllwvpgstgdivltqspgtlslspgeratlsckasqsvdydgdsymnwy}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            apoptosis; HFE7A; autolumune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogrem syndrome; pernitious anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autolumune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; Insulin-dependent diabetes; allergy; atopy; arteriosclesols; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
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Pred. No. 2.5e-64;
1; Mismatches 6; Indels 0:
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Best Local Similarity 97.1%;
Matches 231; Conservative
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Location/Qualifiers

Key

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Gaps

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Length 238;

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This is the amino acid sequence of the PDHH type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAN80342) entabled making DIE, P47A, K49R, H80S, P81R, V82L, E84P, A81F, T89V and R107K amino acid substitutions; these residues are conserved in the human light chain (kappa chain). Host cell Escherichia coli pHSHH5 SANK 70398 harbors plasmid pHSHH5 carrying a fusion fragment of the humanised PDHH type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BP-6274 (claimed). The invention provides methods for producing humanised antibodies by culturing host energy methods for inducing apoptosis in abnormal cells.

Expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of dissesses that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythemacosus, Hashimoto's disease, carefurlitis, autoimmune haemolytic anaemia, disease, rheumatoid arravis, multinen haemolytic anaemia, sterility, mvashbenia gravis, multinen haemolytic anaemia, m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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, Tohru T;
                     /label= Sig_peptide
21..238
/label= Mat_protein
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                                                                                                         'label- Variable
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/label= Constant
                                                                                                                                                                                                                "claim 9"
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/note= "claim 9"
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/note= "claim 9"
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/label= CDR_L1
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N-PSDB; AAV70077.
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25-JUN-1997;
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238 AA;

Sequence

(complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, applementals, apparatic anaemia (pannyalpohthisis), hepatitis, AIDS and organ graft rejection. Sequences ABB14772-B14774 and AAB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region: CDR; human Fas; Fas Ilgand, Apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft@reficention; light chain. The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fassantibody as the active component. The anti-Fas antibody is either the murine anti-luman Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody - $\frac{2}{3}$ 121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180 QQKPGQAPRLLIYAASNŒESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120 1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60 181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 Indels Humanised anti-Fas antibody light chain, SEQ ID NO:107. Score 1201; DB 19; Pred. No. 2.8e-64; 3; Mismatches 5; Claim 20; Page 101; 139pp; Japanese. AAB14777 standard; Protein; 238 AA. 96.48; 96.68; 99JP-0278301. 98JP-0276883. 24-NOV-2000 (first entry) Conservative Chimeric - Homo sapiens Chimeric - Mus musculus (SANY) SANKYO CO LID. WPI; 2000-485645/43. N-PSDB; AAA72176. Similarity JP2000169393-A. 30-SEP-1999; 30-SEP-1998; 20-JUN-2000. Matches 230; AAB14777; Query Match Best Local RESULT 14 61 AAB14777 ŏ a δy Op ò Pp A NAME OF A NAME δ g

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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirhematic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarcitis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                            121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                                                                        QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                        Gaps
                                                                                                                                 1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                                 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                 New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively icells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel humanized anti-Fas antibody-like
                                                                                                       ;
                                                                         21; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takahashi
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tamaki I,
                                                                       Score 1201; DB 21
Pred. No. 2.8e-64;
3; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised HFE7A designed light chain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 141-142; 263pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                       AAW90927 standard; Protein; 238 AA.
                                                                         96.4%;
96.6%;
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98JP-0276882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2000 (first entry)
                                                                       Query Match 96.4
Best Local Similarity 96.6
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serizawa N, Haruyama H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-258930/23.
                            238 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1998;
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 antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW90927;
                               Sequence
                                                                                                                                                                                                                                                                                                                181
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molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
apoptosis in cells withia normal system, by inhibiting binding between
Fas and its ligand. The products of the invention have anti-inflammatory,
anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosuppressive, thyromimetic,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, saforgen's syndrome, permicious or hypoplastic
cheases associated with the Fas/Fas ligand system, especially systemic
clupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
corress, host disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
colls. They bind to both human and murine Fas, so can be evaluated in
murine disease models: (I) act on the active site of Fas, i.e. they mimic
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models: (I) act on the active site of Fas, i.e. they mimic
change a human anti-murine antibody response. This sequence represents
a humanised anti-ras antibody HegyA designed light chain which is used in ő 121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180 61 QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLT1HPVEEEDAATYYCQQSNEDPR 120 Gaps 9 1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60 181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238 ; 0 Length 238; Indels Score 1201; DB 21; Pred. No. 2.8e-64; 3; Mismatches 96.48; 230; Conservative Local Similarity 238 AA; Sequence Query Match Matches 61 181 셤 δ g ò g ò

Search completed: April 24, 2002, 15:09:52 Job time: 95 sec

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(without alignments)
127.276 Million cell updates/sec
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1 METDIILLWYLLLWYPGSTG......EVTHQGLSSPVTKSFNRGEC
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/FB_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     212252 seqs, 22503292 residues
                                                                                                                     April 24, 2002, 15:10:40;
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Maximum Match 100%
Listing first 45 summaries
                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
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Sequence:
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli	13,	σ	Н	Sequence 13, Appl	1, 1	٦,	15,	17,	19,	24,	15,	17,	19,	24,	15,	17,	19,	24,	26,	6, A	o,	25,	25,		97,	39,
SUMMAKIES	ID	PCT-US96-13152-2	US-08-887-352B-13	US-08-466-151-9	US-09-109-207C-13	US-09-296-005-13	US-09-282-505-1	US-09-054-255-1	US-08-887-352B-15	US-08-887-352B-17	US-08-887-352B-19	US-08-887-352B-24	US-09-109-207C-15	US-09-109-207C-17	US-09-109-207C-19	US-09-109-207C-24	US-09-296-005-15	US-09-296-005-17	US-09-296-005-19	US-09-296-005-24	US-07-916-098A-56	US-08-487-550-6	US-09-049-672A-6	US-07-934-373C-25	. US-08-437-642B-25	PCT-US93-07832-25-	US-09-171-945-97	US-07-934-373C-39
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	Length DB	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	218	241	239	234	233	233	233	235	214
d	Query Match	82.8	81.7	81.7	81.7	81.7	79.9	79.9	79.6	79.6	79.6	79.6	79.6	79.6	9.62	79.6	9.62	9.6	79.6	9.64	77.8	77.5	77.0	75.5	75.5	75.5	75.5	75.2
	Score	1032	1018	1018	1018	1018	995	995	866	992	992	992	992	885	992	992	992	892	992	992	969.5	965.5	959	940.5	940.5	940.5		937
	Result No.	1	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 39, Appl Sequence 153, Appl Sequence 153, Appl Sequence 153, Appl Sequence 153, Appl Sequence 154, Appl Sequence 175, Appl Sequence 11, Appl Sequence 11, Appl Sequence 2, Appli Sequence 2, Appli Sequence 10, Appl Sequence 10, Appl Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	for prevention of multiple organ
214 3 US-08-437-642B-39 235 1 US-08-29-07832-39 235 1 US-08-29-575-153 235 1 US-08-899-575-153 235 1 US-08-899-575-153 235 5 PCT-US95-08743-153 235 5 PCT-US95-08743-153 236 2 US-09-171-98-99 214 3 US-09-171-88-800-11 214 4 US-09-097-171A-2 214 5 PCT-US93-07832-4 237 4 US-09-097-171A-10 237 4 US-09-097-171A-10 237 4 US-09-097-171A-10 237 4 US-09-097-171A-10 237 4 US-09-097-171A-10	ALIGNMENTS 9613152 et al. electin antibodies ble //MS-DOS US96/13152 US96/13152 5 112 895.8 5 112 895.8 5 114 969.9 946 BOER 1059-PCT-PFE/ON:
28 937 75.2 29 33.5 5 75.1 22 33 935.5 75.1 22 33 935.5 75.1 22 33 935.5 75.1 22 33 935.5 75.1 22 34 932.5 74.8 22 44 932 74 932 74 932 74 932 74 93 7	RESULT 1 PCT-US96-13152-2 Sequence 2, Application RG/TUS96 GENERAL INFORMATION: APPLICANT: Martin, Ulrich, e TITLE OF INVENTION: Apti-sel, NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: Felfe & Lynch ADDRESSEE: Attn: Norman D. STREET: 805 Third Avenue CITY: New York COUNTRY: U.S.A. ZITE: 1002-2 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/M SOFTWARE: ASCII COMPUTER: ASCII C

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121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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TOPOLOGY:
US-08-466-151-9
                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                       US-08-466-151-9
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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                                                                                                                   IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                         GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 218;
   11; Indels
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                                                                                                                                                                                                                                       201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                            Score 1018; DB 2;
Pred. No. 1.3e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
   11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.7%; Score Lory,
88.5%; Pred. No. 1.3e
tive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILLIO DATE: 03-Jul-1997
CLASSIFCATION: 530
                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08887352B
Patent No. 5994511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: SVODOda, Craig G.
REGISTRATION NUMBER: 39,044
REFRENCE/CDOCKET NUMBER: P112:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-1489
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: J DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 218 amino acids
Amino Acid
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94080
                                                                                                                                                                                                                                                                                                                                         US-08-887-352B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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21 DIVLIQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.7%; Score 1018; DB 3;
88.5%; Pred. No. 1.3e-77;
11ve 13; Mismatches 12;
201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                    E: 3.5 inch, 1.44 Mb floppy disk IBM PC compatible
                                                                                                                                                                                                              APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
WIMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESSE
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P0718P2C1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION
APPLICATION NUMBER: *08/466163
FILING DATE: 06-Jung1995
APPLICATION NUMBER: *08/405617
FILING DATE: 15-MARE1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: *08/185899
FILING DATE: 26-JAN1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: *07/879495
FILING DATE: 07-MAY;1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: *07/874495
PRIOR APPLICATION DATA:
APPLICATION NUMBER: *07/8747992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                             Sequence 9, Application US/08466151 Patent No. 6037453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 81.7%
Best Local Similarity 88.5%
Matches 193; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                       California
: USA
                                                                                                                                                                                                                                                                                                                                            1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino Acid
                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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us-09-499-662-52.rai

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81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                 81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                          141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                  Gaps
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                                                                                              Length 218;
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                       chain sequence derived from MAE11
                                                                                                                              12; Indels
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                                                                                            ;; Score 1018; DB 4;
;; Pred. No. 1.3e-77;
13; Mismatches 12;
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APPLICANT: Esche Ekinaduese Idusogie et al.
TITLE OF INVENTION: POLYPEPTIGE Variants
FILE REFERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
LENGTH: 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/09282505A; Patent No. 6194551
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ORGANISM: Artificial Sequence
                                                                                            81.7%;
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                                                                                            Query Match
Best Local Similarity 88.5
Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 86.7 Matches 189; Conservative
                   ; OTHER INFORMATION: Light US-09-296-005-13
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 LOCATION: 1-218
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US-09-282-505-1
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US-09-054-255-1
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Fatent No. 6290957
GENERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION UNBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                            APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P1123R1 CURRENT PILLOR NUMBER: US/09/109, 207C CURRENT FILLING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/051,554 PRIOR FILLING DATE: 1997-07-03 NUMBER OF SEQ ID NOS: 44 SEQ ID NOS: 44 LENGTH: 218
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 141 IFPPSDEOLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                       121 IFPPSDEQLKSGTASYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Light chain sequence derived from MAEll
US-09-109-207C-13
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                                                                                            201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                         ; Sequence 13, Application US/09109207C
; Patent No. 6172213
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Best Local Similarity 88.5%
Matches 193; Conservative
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ORGANISM: Artificial
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                                                                                                                                                                                     US-09-109-207C-13
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US-09-296-005-13
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LENGTH: 218
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Sequence 17, Application US/08887352B Patent No. 5994511 GENERAL INFORMATION:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: SYODOGA, CRAIGG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P112
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPHONE: 650/925-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 DNA way
CITY: South San Francisco
STATE: California
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CLASSIFICATION: 530
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Amino Acid
                                                                                                     Query Match 79.6%
Best Local Similarity 86.2%
Matches 188; Conservatiwe
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentect
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-15
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Best Local Similarity
Matches 188; Conserv
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Fatent No. 5994511

GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                               Length 218;
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                                                                                                                                                                                                                                                            ; OTHER INFORMATION: E27 anti-IgE antibody light chain US-09-054-255-1
                                                                                                                                                                                                                                                                                                                                           79.9%; Score 995; DB 4;
86.7%; Pred. No. 1e-75;
live 15; Mismatches 14
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266
CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT FILING DATE: 1998-04-02
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
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FILING DATE: 03-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity 86.7<sup>1</sup>
Matches 189; Conservative
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US-08-887-352B-15
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
WUMBER OF SEQUENCES: 26
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Length 218;
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79.6%; Score 992; DB 2; Length 21
86.2%; Pred. No. 1.8e-75;
iwe 16; Mismatches 14; Indels
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ilarity 86.2%; Pred. No. 1.8e-75;
Conservative 16; Mismatches 14.
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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-igE Antibodies and Method of Improving Polypep
FILE REFERENCE: P1123R1
                                                      Sequence 24, Application US/08887352B

Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-19E Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES. 26
CORRESPONDENCES. 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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86.2%; Pred. No. 1.8e-75;
Live 16; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Ju1-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,
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Amino Acid
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Best Local Similarity 86.2'
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                 94080
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US-08-887-352B-24
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US-09-109-207C-15
                                       US-08-887-352B-24
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                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/08887352B
Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                   IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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COMPUTER READBLE FORM: 1.44 Mb floppy disk
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPATIDLE
COMPUTER: TRM PC COMPATIDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WinPatin (Generated)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
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CITY: South San Francisco
STATE: California
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OPERATING SYSTEM:
SOFTWARE: WinPati
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US-08-887-352B-19
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept FILE REFERENCE: P1123R1*
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR PRIOR PAPLICATION NUMBER: 05 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEO ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypept FILE REFERENCE: P1123R1 CURRENT APPLICATION NUMBER: US/09/109,207C CURRENT APPLICATION NUMBER: US 60/051,554 PRIOR APPLICATION NUMBER: US 60/051,554 NUMBER OF SEQ ID NOS: 44
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        121 IFPPSDEQLKSGTASVVÇLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 1-218
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19
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86.2%; Pred. No. 1.8e-75;
Live 16; Mismatches 14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 188; Conservative
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Best Local Similarity
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LENGTH: 218
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LENGTH: 218
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Patent No. 6172213
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTYON: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109, 207C
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1999-06-30
PRIOR FILING DATE: 1997-07-03
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                                                   SEQ ID NO 15
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial
FEATURE: NAME/KEY: Artificial
LCCATION: 1-218
COTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: Artificial
; LCCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-17
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PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1997-07-03 NUMBER OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.2*
Matches 188; Conservative
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SEQ ID NO 17
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ORGANISM: Artificial
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US-09-109-207C-17
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ö Gaps ; 0 Query Match 79.6%; Score 992; DB 4; Length 218; Best Local Similarity 86.2%; Pred. No. 1.8e-75; Matches 188; Conservative 16; Mismatches 14; Indels 201 qq ò Dp δy g δ

Search completed: April 24, 2002, 15:10:40 Job time: 143 sec

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protein search, using sw model OM protein Run on:

April 24, 2002, 15:11:36; Search time 49.97 Seconds (without alignments) 362.809 Million cell updates/sec

US-09-499-662-52 1246 1 MEIDTILLMVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 segs, 76174552 residues

Searched:

length: 0 length: 2000000000 sed Minimum DB : Maximum DB :

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

pir1:*
pir2:*
pir3:*
pir4:* PIR_68:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ig kappa chain NIG Ig kappa chain NIG Ig kappa chain NIG Ig kappa chain Am3 Ig kappa chain Am3 Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain Pre Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain - m Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain V r Ig kappa chain Dre Ig kappa chain Dre Ig kappa chain pre Ig lambda-like cha Description SUMMARIES S68241 JC5810 \$38865 \$25058 \$42772 \$16112 JE0241 S06084 \$14237 \$33161 PC4203 \$52028 \$37484 \$68212 \$01320 JL0029 PT0219 PH1226 S29593 A56169 Query Match Length DB 54.4 48.7 488.7 448.7 447.5 445.4 962.5 927.5 902.5 900.5 878 Result So.

Grappa chain NIG2 precursor - human C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 05-Dec-1998 #text_change 21-Jan-2000
C; Accession: JE0344
R; Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H S; Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H A; Description: A new subgroup of k type light chains (VkV) identified in cases of AL A; Reference number: JE0344
A; Reference number: JE0344
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-215 <ALL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology

S52059 A20969

RESULT JE0244

C r	pre	pre	pre	pre	ر ر	V r	V r	C r	V r	V r	я -	V r	CF	V r	pre	
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КЗНО	KVMSM	PN044	S5502	KVMS32	S2063	KVMS4	KVMS8	A3792	KVMS0	S1997	S2957	KVMS6	S2665	KVMSC	кзнин	
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106	131	140	131	132	145	111	111	66	111	112	233	111	66	111	129	
44.0	44.0	43.5	42.8	42.5	42.0	41.5	41.3	41.2	41.2	41.1	41.0	40.9	40.7	40.3	40.2	
548	548	542	533	529	523.5	517	515	513	513	512	511	510	507	502	500.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Typectes: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accesion: JED042
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinod submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: A;Reference number: JED242
A;Reference number: JED242
A;Residues: 1-215
A;Residues: 1-215
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                             Length 215;
                                                                                                                                                                                                                                                                                                                                                             77.2%; Score 962.5; DB 2; Length 86.2%; Pred. No. 5.1e-56; Live 11; Mismatches 16; Indels
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Best Local Similarity 86.2%
Matches 188; Conservatlye
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Gaps

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Length Indels

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homology

immunoglobulin

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GIPDRESGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                                                                                                                        Score 900.5; DB 2
Pred. No. 5.5e-52;
; Mismatches 23
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
C;Superfamily: immunoglobulin V region; immuno
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>
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ilarity 84.3%;
Conservative
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Best Local Similarity
Matches 183; Conserv
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Best Local Similarity
Matches 174; Conserv
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE024
S;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; submitted to JIPID, November 1998
A;Berence number: JE0243
A;Reference number: JE0243
A;Reference number: JE0243
A;Rocession: JE0243
A;Rocession: JE0243
A;Rocession: JE0243
A;Rocession: JE0243
A;Rocession: JE125 AALLY
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                        Length
                                                                                           Indels
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                                      Score 927.5; DB 2; Pred. No. 9.6e-54; Pred. no. 9.6e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ig Kappa chain V-III (KAU cold agglutinin) - human C; Species: Homo sapiens (man) C; Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #te. C; Accession: A23746 R; Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B. J. Biol. Chem. 266, 2836-2842, 1991 A; Title: The primary structure of the Fab fragment of A; Reference number: A23746; MUID:91131575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.4%; Score 902.5; DB 2; Best Local Similarity 81.7%; Pred. No. 4e-52; Matches 179; Conservative 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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                                                                                       10; Mismatches
     <IMM>
   F;16-90/Domain: immunoqlobulin homology
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                                                      74.48;
84.08;
                                                                                         Matches 184; Conservative
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Best Local
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Ig kappa chain Am37 precursor - human cispeciaes: Homo sapiens (man) C. Dactelses: Homo sapiens (man) C. Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C. Accession: JE0241 Yamanki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIPID, November 1998 A. Description: Structure relationship of kappatype light chains with AL amyloidosis: A. Recession: JE0241 A. Recession: JE0241 A. Molecule type: protein A. Molecule type: protein A. Recession: JE0241 A. Secondalius: 1-216 CALI C. Superfamily: immunoglobulin V region; immunoglobulin homology F;16-92/Domain: immunoglobulin homology <IMM>
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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monoclonal antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: JG5810
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Blochem Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porpare reference number: JG5810; MUID:98063277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JC5810
A; Molecule type: protein
A; Residues: 1-218 <AKA.
C; Comment: This catalytic antibody has peroxidase oxidase. It is directed against a F; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      If Kappa chain V region (clone 23.2) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C; Accession: A56169
R; Monfardini, C: Kieber-Emmons, T:; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Go. J. Biol. Chem. 270, 6628-6638, 1995
A; Title: Recombinant antibodies in bloactive peptide design.
A; Reference number: A56169; MuID:95204454
A; Accession: A56169
A; Status: preliminary; not compared with conceptual translation
     141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                                                                      IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.1%; Score 774; DB 2; Length 21 ilarity 66.5%; Pred. No. 9.3e-44; Conservative 28; Mismatches 45; Indels
                                                                                                                                                                                                                                 60.9%; Score 759; DB 2;
68.4%; Pred. No. 8.5e-43;
11ve 26; Mismatches 40;
                                                                                                                                                                                                 201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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Best Local Similarity 68.49
Matches 143; Conservative
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Best Local Similarity
Matches 145; Conserva
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                               61
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A.Residues: 1-218 <TAK>
A.Residues: 1-218 <TAK>
A.Cross-reneces: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
A.Cross-reneces: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
R.Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A.Title: Thermostable Peroxidase activity with a recombinant antibody L chain-porphyrin
A.Reference number: S68211; MUID:96085223
A.Accession: S68214
A.Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   If Kappa chain V region (Mabl3-1) - mouse (fragment)
N.Alternate names: immunoglobulin light chain
N.Alternate names: immunoglobulin light chain
C.Specias: Mus musculus (house mouse)
C.Specias: Augu-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C.Accession: 568214; 568214
R.Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.submitted to the EMBL Data Library, March 1994
A.Description: Specific peroxidase activity by formation of an antibody L-chain-porphyriterence number: 568241
                                                            rat myeloma immunoglobulin kappa chain cDNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 PRTFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 178
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                                                                                                        A, Accession: S06084
A: Molecule type: mRNA
A: Molecule type: mRNA
A: Molecule type: mRNA
A: Molecule type: mRNA
A: Residues: 1-240 CRD>
A: Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
C: Superfamily: immunoglobulin V region; immunoglobulin homology
C: Reywords: heteroretramer; immunoglobulin
F: 1-20/Domain: signal sequence #status predicted <SIG>
F: 21-240/Product: Ig kappa chain #status predicted <MAT>
F: 153-222/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                    63.8%; Score 795; DB 2;
62.5%; Pred. No. 4.4e-45;
tive 35; Mismatches 53
R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A;Title: Nucleotide sequence of Y3-Ag 1.2.3.
A;Reference number: S06084; MUID:90016888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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A; Residues: 'NI', 3-212 <TAW>
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Best Local Similarity
Matches 150; Conserv
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nes 144; Conserv
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Indels

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56

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Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (domestic sheep)
#text_change 20-Jun-2000
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                                                                                                                                                                                                                                            QQKPGQAPRLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                     TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 QAPKLLIYYATRLHTDVPSRFSGSGSGTDYTLTISNLEANDTATYYCLQYESTPLAFGGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 TRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 LLWVLLLW-VPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                Ig kappa chain - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-
C:Accession: S33161
R;Foley. R.C.; Beh, K.J.
submitted to the EMBL Data Library, July 1990
A;Description: Isolation and characterisation of sheep kappa light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A. Molecule type: mRNA
A. Residues: 1-230 <FOLD.
A.Cross-references: EMBL.X54110; NID:9297103; PIDN:CAA38046.1; E
S. Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;143-212/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                             , DB 2; L
9.3e-40;
ches 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.2%; Score 712.5; DB 2
58.4%; Pred. No. 9.8e-40;
1ive 38; Mismatches 54
                                                             Score 713; DB Pred. No. 9.3e-7; Mismatches
      F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                 37;
                                                             57.2%;
                                                                                                   Conservative
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A; Status: preliminary
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Best Local Simi
Matches 136;
                                                                                                   Matches 134;
                                                               Query Match
Best Local
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C'Specides: Mus musculus (house mouse)
C'Specides: Musculus (house mouse)
C'Specides: Musculus (house mouse)
C'Specides: Musculus (house mouse)
J. Biol. Chem. 263, 17100-17105, 1988
A'Title: Preliminary crystallographic data, primary sequence, and binding data for a A'Reference number: A92686; MUID:89034213
A'Reference number: A92686; MUID:89034213
A'Recession: A31790
A'Molecule type: mRNA
A'Residues: 1-220 ASGH>
A'Residues: 1-220 ASGH>
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A'Residues: 1-220 ASGH>
A'Residues: 1-220 ASGH>
C'SCH>
C'Superfamily: immunoglobulin V region; immunoglobulin homology
C'Reywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
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                                                                             GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                             141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                 139 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 198
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DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES
                        1 DIVLTQSPASLTVSLGQRATISCRASKSVSSGGYSYMHWYQQKPGQPPKVLIYLASNLES
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Pred. No. 4.8e-40;
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STLTLTKDEYERHNSYTCEATHKTSTSPI 209
                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V region (17/9) - mouse
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Best Local Similarity 60.59
Matches 133; Conservative
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A; Residues: 1-234 <VAN>
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R; van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.; Submitted to the EMBL Data Library, August 1994
A;Description: Coordinate expression of antibody subunit genes yields high levels of fun A;Reference number: S52028
A;Accession: S52028
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                                                 A; Accession: PC4203
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
C; :Title: Cloning and characterization of cDNAs coding for heavy and light chains of A:Reference number: PC4202; MUID:97082978
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C.Date: 07-May_1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
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A; Residues: 1-219 <VAN>
A; Cross-references: EMBL:135138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 60.3%; Pred. No. 3.1e-39;
Matches 132; Conservative 35; Mismatches 51
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Ig kappa chain - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Was musculus (house mouse)
C.Species: 06-Jan 1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C.Accession: S37484
R.Ducancel, F.F.D.
A.Rocession: S37484
A.Reference number: S37483
A.Recession: S37484
A.Status: preliminary
A.Resiques: 1-225 < DUC>
A.Resiques: 1-225 < DUC>
A.Resiques: 1-225 < DUC>
C.Superfamily: immunoglobulin v region; immunoglobulin homology
C.Superfamily: immunoglobulin v region; immunoglobulin homology
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Matches 137; Conservative
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Search completed: April 24, 2002, 15:11:37 Job time: 195 sec

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April 24, 2002, 15:13:45; Search time 29.21 Seconds (without alignments) 298.741 Million cell updates/sec
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GenCore version
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Query Match
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                                                                                                                                                                                                                                                                                                   Science 169:56-59(1970).
-!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                   Titani K., Shinoda T., Putnam F.W.; "The amino acid sequence of a kappa type Bence-Jones protein. 3 complete sequence and the location of the disulfide bridges."; Biol. Chem. 244:3550-3560(1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH A HEAVY CHAIN).

V -> L (IN INV(1,2) MARKER).

/FTIG=VAR_003897.

D -> N (IN REF. 7 AND 8).

E -> Q (IN REF. 5 AND 6).

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Kohler H., Shimizu A., Paul C., Putnam F.W.;
"Macroglobulin structure: variable sequence of light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 106;
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  Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11arity 100.0%; Score 548; DB 1; 100.0%; Pred No. 3.6e-38; Conservative 0; Mismatches 0;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 03, Last annotation update)
IG KAPPA CHAIN V-III REGION MOPC 63 PRECURSOR
                                                                                                                                                                                             SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
                                          SEQUENCE (BENCE-JONES PROTEIN AG)
MEDLINE-69234734; PubMed-4893682;
                                                                                                                                                                                                                                                                                                                                                                         MARKER, 45-ALA AND 83-LEU.
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57 E
11609 MW;
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InterPro; IPR003597; Ig_cl.
Pfam: PF00047; Ig; 1.
SMART: SM00407; IGcl.
PROSITE: PS00290; IG_MHC; 1.
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MEDINE=79012520; PubMed=99744;
MCKean D.J., Bell M., Potter M.;
McKean D.J., Bell M., Potter M.;
Machanisms of antibody diversity; multiple genes encode structurally related mouse kappa yariable regions.";
Proc. Natl. Acad. Sci. J. 75:3913-3917(1978).
PIR, A01935; WKWSMG.
InterPro; IPR003006; j.g_MHC.
InterPro; IPR003066; j.g_MHC.
InterPro; IPR0047; 19: 1:
PFam; PF00047; 19: 1:
SMART: SM00406; IGv; 1.
Immunoglobulin v region; Signal.
SIGNAL.
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MEDLINE=73140225; PubMed-4691517;
MEDLINE=73.40225; PubMed-4691517;
MCKean D.3., Potter M., Hood L.E.,
"Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";

Biochemistry 12:760-771(1973).
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              Burstein Y., Schechter I., "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";
Biochemistry 17:239222400(1978).
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MEDLINE=78235887; PubMed=98179;
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Eukaryota; Metazoa; Cl
Mammalia; Eutheria; R
NCBL_TaxID=10090;
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131 AA;
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SEQUENCE OF 1-37.
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                           Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                     GIPARFSGSGSGTDFTLAIHPVEBEDAATYTCQOSNEDPFTFGSGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                          GIPDRESGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIK 131
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Pred. No. 1.3e-35;
7; Mismatches 7; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III:REGION PC 7183.
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86.5%;
              PIR, A01937, KVMS43.
InterPro, IPR003006, Ig_MHC.
InterPro, IPR003596; Ig_V.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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1 Similarity 87.4%;
97; Conservative
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Nature 276:785-790(1978).
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SMART; SM00406; IGv; 1.
Immunoglobulin V region
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-!- HISCELLANGOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROPEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
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                                                                                                                SEQUENCE OF 21-132.
MEDLINE=73140224; PubMed-4120629;
MCKean D.J., Potter M., Hood L.E.;
"Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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            Burstein Y., Schechter I.; "Primary structures of N-terminal extra peptide segments linked the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled
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15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 7043.
MUS musculus (Mouse).
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Biochemistry 17:2392-2400(1978).
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MEDLINE=78235887; PubMed=98179;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                       MEDLINE=79073152; PubMed=103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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                                 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIK 131
                                            81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIK 131
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1 Similarity 86.5%; Pred. No. 2.7e-35;
96; Conservative 7; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                         MW; 7A4ADE4D6C256D29 CRC64;
                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
RAPPA CHAIN V-III REGION PC 6308.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FU30_MOUSE STANDARD; PRT; 111 AA. P01669; Cal-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 16-JUL-1999 (Rel. 38, Last annotation update) Mus musculus (Mouse).
                                                                                                111 AA
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PIR; C01937; KVMSOB.
InterPro; IPR003806; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
                                                                                                 STANDARD;
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38
53
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111
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Best Local Similarity
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KV3Q_MOUSE
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McKean D.J., Bell M., Potter M.; "Mechanisms of antibody diversity: multiple genes encode structurally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 510; DB 1; Length 111;
Pred. No. 4.7e-35;
9; Mismatches 7; Indels
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COMPLEMENTARITY-DETERMINING 2.
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                                                                                                                                                                                                                                                                                                                                                                           6FAA345279356829 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION CBPC 101.
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BY SIMILARITY
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BY SIMILARITY.
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MEDLINE-79012520; Pubmed-99744;
                                                                                                                                                                                                                                                                                                                                                                           12011 MW;
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Mammalia, Eutheria, Rodentia;
                                                                        PIR, E01937; KVMS69.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                  40.9%;
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InterPro; IPR003596; Ig_V.
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                                        diversity.";
Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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SMART; SM00406; IGV; 1.
Immunoglobulin V region
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Matches 95; Conserv
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111 AA;
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Nature 276:785-790(1978).
PIR; D01937; KVMS10. F
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                                                                                                                                                                                                                                                                                                                                Best Local Similarity 84.7
Matches 94; Conservative
                                                       STANDARD;
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38
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100
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SMART; SM00406; IGv; 1.
Immunoglobulin V region
and the state of
                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                   110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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39
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                                                       KV3P_MOUSE
P01668;
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DISULFID
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KV3M_HUMAN
                                                KV3P_MOUSE
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                                                              21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                      1 METDTILLWWLLLWWPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                               somatic
                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.2%; Score 500.5; DB 1; Length 129; 74.2%; Pred. No. 3.3e-34; live 12; Mismatches 19; Indels 3:
                                                                                                    IG KAPPA CHAIN V-III REGION HAH
                                                                                            81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIK 131
                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
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                                  Length 111;
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                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MW; D3C55292772774D0 CRC64;
                                 Score 502; DB 1; I
Pred. No. 2.1e-34;
9; Mismatches 8;
                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-UUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
                                                                                                                                                129 AA
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PIR: PLOD22; K3HUHA.

HSSP; P01789; 2MCP.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_V.

Ffam; PP00047; ig; 1.

SMART; SM00406; IGv; 1.
                                ch 40.3%;
l Similarity 84.7%;
94; Conservative
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14073 1
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                                                                                                                                                                                            Homo sapiens (Human).
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129 AA;
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                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                              KV3L_HUMAN
P18135;
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                                 Query Match
Best Local S:
Matches 94
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SEQUENCE
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Best Local 9
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Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
Mattoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).
J. DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.5%; Score 492.5; DB 1; 84.7%; Pred. No. 1.2e-33; Live 8; Mismatches 8;
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P18136.
P18136.
D10N-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11G KAPPA CHAIN V-III*REGION HIC PRECURSOR.
HOMO Sapiens (Human).
                                                21-JUL-1986 (Rel. 01 Created)
21-JUL-1986 (Rel. 01 Last sequence update)
12-JUL-1999 (Rel. 38% Last annotation update)
IG KAPPA CHAIN V-III%REGION PC 7210.
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BY SIMILARITY
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111 12039 MW; 1E46988341858526 CRC64;

111 AA;

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KV3K_HUMAN
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                                                                                                                                                                                                                                            1 METDTILLMVLLLMVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-79073152; PubMed-103003; Welgert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                   3;
                                                                                                                                                                                                  DB 1; Length 129;
                                                                                     KAPPA CHAIN V-III REGION HIC.
                                                                                   IG KAPPA CHAIN V-III REGION HIG FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
                                                                                                                                    COMPLEMENTARITY-DETERMINING 3, JK1 SEGMENT.
BY SIMILARITY.
                                                                                                             FRAMEWORK 2. COMPLEMENTARITY-DETERMINING 2.
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FRAMEWORK 3.
COMPLEMENTARITY-DETERMINING 3.
FRAMEWORK 4.
BY SIMILARITY.
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                                                                                                                                                                                               Query Match 39.1%; Score 487.5; DB 1; Length Best Local Similarity 72.7%; Pred. No. 3.8e-33; Matches 96; Conservative 12; Mismatches 21; Indels
                                                                                                                                                                         7395528EA2BB74D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                 111 AA
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                                                                                                                               FRAMEWORK 3.
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               PIR; PLO021; K3HUHI.
HSSP: POLT99; ZUCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Fam; PF00047; ig; 1.
SMART; SMO0407; ig; 1.
                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A01938; KVMS84.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
                                                                                                                                                                        14070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diversity.";
Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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129
43
55
70
77
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38
53
60
101
111
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                                                                                                                                                                                                                                                                                                               129
129 AA;
         LEUKEMIA.
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P01670;
                                                                                                                                                      DISULFID
NON_TER
SEQUENCE
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DISULFID
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KV3R_MOUSE
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                                                    Gaps
                                                                                              21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-86641852; PubMed-2997711;
Klobeck H.G., Meindl'A., Combriato G., Solomon A., Zachau H.G.;
"Human immunoglobulim". Kappa light chain genes of subgroups II and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Erimates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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  Length 111;
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COMPLEMENTARITY-DETERMINING
JKI SEGMENT.
BY SIMILARITY.
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                                                 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 FRAMEWORK 3.
117 COMPLEMENTARITY-DETERMINI)
128 JKI SEGMENT.
108 BY SIMILARITY.
128 JKI CC8957F0FE3B9012 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION IARC/BL41 PRECURSOR.
Homo saplens (Human)
ch 36.4%; Score 454; DB 1; I Similarity 77.5%; Pred. No. 1.7e-30; B6; Conservative 11; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.4%; Score 453; DB 1;
69.7%; Pred. No. 2.4e-30;
iive 13; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                 128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              III.";
Nucleic Acids Res. 13;6499-6513(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 200021; CAA77316.1; -.
PIR; A01899; K3H041.:
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Fami; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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128
128 AA;
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Best Local Similarity
Matches 92; Conserv
                           Best Local Similarity
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    Query Match
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SEQUENCE
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SEQUENCE (TEPC 111).
MEDLINE-79012520; PubMed-99744;
MECHANISMS of Antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-1. MISCELLANBOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Wataryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE (PC 3741).
MEDLINE=79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAMEWORK 3. COMPLEMENTARITY-DETERMINING 3.
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                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
                                                                                                                                                                                                                                                                         111 AA
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InterPro: IPR003596; Ig_v.
Pfam: PF00047; Ig; 1.
SMART: SM00406; IGv; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                       121 TFGQGTRLEIKR 132
                                                                                                                                  117 TFGQGTKLEIKR 128
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                                                                                                                                                                                                                    RESULT 14

KV3H_MOUSE

AC POIGGO;

DT 21-JUL-1996

DT 21-JUL-1996

DT 15-JUL-1996

DF 12-JUL-1996

OS MURS MUSCULUS

OC EUKARYOLE; M.

AMMENTIA; EU

OX MAMMATIA; EU

OX MEDLINE=7907

RA WEJCELLE

RY REATYANGEN

RY REATYANGEN

RY REATYANGEN

RY MEDLINE=7907

RY MEDLINE=7907

RY MEDLINE=7907

RY MEDLINE=7907

RY MECHANISMS

RY MECHANISMO

RY MART; SMOO

DR SMART; SMOO

FT DOMAIN

FT TOMAIN

FT TOMA
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KV3S_MOUSE
ID KV3S_MC
AC P01671;
DT 21-JUL-
                                                         57
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Gaps
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                                          Mus musculus (Mouse).

Eukaryotai Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE-79073152; PubMed=103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIK 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.8%; Score 446; DB 1; Length 11 Best Local Similarity 75.7%; Pred. No. 7.5e-30; Matches 84; Conservative 12; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12010 MW; F041E89AA7858523 CRC64;
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-III;REGION PC 7175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK 4.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK 2.
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PIR, B01938; KVMS75.
InterPro; IPR003006; SIg_MHC.
InterPro; IPR003596; Sig_V.
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SEQUENCE
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Search completed: April 24, 2002, 15:13:45 Job time: 322 sec

us-09-499-662-52.rsp

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 24, 2002, 15:13:10; Search time 86.76 Seconds

(without alignments)

401.254 Million cell updates/sec

1246
Sequence: US-09-499-662-52
Sequence: 1246
Sequence: LABEDTILLWVLLIWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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SPTREMBL_17:*

1: sp_arches:*
2: sp_barches:*
3: sp_fungi:*
4: sp_hunan:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plane:*
11: sp_rodent:*
12: sp_virus:*
13: sp_virus:*
14: sp_unclassified:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O99m37 musculu	mus		Ogul78 homo sapien	Ogul86 homo sapien	09ul77 homo sapien	091180 mus musculu	09ul79 homo sapien	Ogul70 homo sapien	Ogul83 homo sapien	Ogul85 homo sapien	Q9ul81 homo sapien	09ul80 homo sapien	09u410 schistosoma	O9erz9 musculu	091174 mus musculu	091178 mus musculu	091176 mus musculu	091182 mus musculu
	ID	Q99M37	Q9R1A5	Q99M11	09UL78	09UL86	Q9UL77	09JL80	09UL79	Q9UL70	O9UL83	Q90L85	Q9UL81	Q9UL80	Q9U410	Q9ERZ9	09JL74	Q9JL78	09JL76	Q9JL82
	DB	; ;	11	11	4	4	4	11	4	4	4	4	4	4	Ŋ	11	11	11	11	11
	Query Match Length DB	238	214	235	109	109	108	103	108	108	108	109	107	114	106	107	66	101	97	104
dР	Query Match	59.8	54.6	34.4	34.2	31.6	31.5	31.4	30.9	30.7	30.6	29.9	29.7	28.6	28.0	26.9	26.4	26.3	26.2	25.8
	Score		680	428.5	426.5	393.5	392	391	385	383	381	372.5	370.5	356	349.5	335	329	328	327	321.5
	Result No.	1	7	m	4	S	9	7	80	6	10	11	12	. 13	14	15	16	17	18	19

0994f0 mus musculu 09184 mus musculu 090184 mus musculu 090182 homo sapien 090829 homo sapien 090829 homo sapien 090829 qinglymostc 0991c4 mus musculu 090807 mus musculu 090807 mus musculu 0997797 mus musculu 099121 mus musculu 099121 mus musculu 099121 mus musculu 09911 homo sapien 09911 homo sapien 099125 mus musculu 09911 homo sapien 099125 mus musculu 09911 homo sapien 099125 mus musculu 09911 homo sapien 099125 mus musculu 09911 homo sapien 099125 mus musculu 09911 homo sapien 099125 mus musculu 09911 homo sapien 09910 homo sapien 09910 homo sapien 09910 homo sapien 09910 homo sapien 09910 homo sapien 09910 homo sapien 09910 homo sapien 09910 homo sapien 09910 homo sapien 09910 homo sapien		AA. update) on update)	Vertebrata; Euteleostomi; Ithi; Muridae; Mus.	/DDBJ databases. 801330A CRC64; . DB 11; Length 238;	, X X	GQAPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEDAATYYCQQSNEDPRTFGQ 124 		SVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
090YF0 09JL84 09JL84 09JUB2 09DR29 09DR29 09DB14 099DL4 099B14 008907 099B14 008907 099B14 008907 099B14 0099UG 099C57 099C52 09	Q90508 ALIGNMENTS	PRT; 238. Created) Last sequence Last annotati	7). ; Craniata; ; Sciurogna	EMBL/GenBank -: FB2B06A0B Score 744.5	TI: Mismatches GTLSLSPGERATLS 1 :	GSGSGTDFTLTIH 		SLSSTLTLSKADYEKHKVYACEV 1: :
4444111111111444		17, 17, 17,	:594 data ntia	the E 5.1; 44 MW;	TOSP TOTP	DRFS DRFS	PSSE	TLSK
・	Anglishasan Mayak U	TINARY; Sirel. Sirel. Sirel.	OR MGC Se) 1, Chor 1, Rode (OR)	26344 26344 25344 259.8	rvative STGDIVL	NLESGIP : NRFSGVP	GTKLEIKRADAAPTVSIFPPS	(SLSSTL
2222 0222		PRELIN (Trem (Trem	orein is (Mous Metazos utheria 10090; OM N.A ARY TUR	JAN-200 035; AJ 238 AA;	37; Conser LWVLLLWVPGS : : LLVLMFWIPAS	LIYAASP LIYKVSP		SVTEODSKDSTY : SWTDODSKDSTY
321 285 285 286 286 287 287 287 287 287 287 287 287 287 287	1/1	37; 37; UN-2001 UN-2001 UN-2001	UNKNOWN (FOYTEIN FORBMGC: 994 MUS musculus (Wouse)) Eukaryota; Metazoa; Chordata Mammalia; Eutheria; Rodentia NCBI_TaxID=10090; [1] SEQUENCE FROM N.A. TISSUB=MAMARAY TUMOR; Stransherg R.	Denitted (BL; BC002) QUENCE Match	137; ILLWVL : VRLLVL	GOAPRI : : GOSPKI GTRIFI	GTKLEI	ESVTEQ : NSWTDQ
01000000000000000000000000000000000000		099M 099M 099M 01-10 01-10	Mus DNKN Mus DNKN Mamma NCBI (1) SEQUI	Subm EMBL SEQUI		65	1 (1)	185
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                                                                                                                                                          Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of CDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           059M11;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:6743).
Whis musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Muscul_TaxID-10090;
                                                                                                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                   54.6%; Score 680; DB 11; Length 214; 58.3%; Pred. No. 3.1e-55; ive 34; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002129; AAH02129.1;
                                                                                                                                                                                                                                                                                                                                                                   52BA205FDE995E2A CRC64;
                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AA.
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                                             01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                              Pfam; PF00047; 19; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_11ke; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                       PRT;
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                                                                                                                                                                                                                                                                                                                                                       214
23922 MW;
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Best Local Similarity 58.33
Matches 127; Conservative
                      PRELIMINARY;
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                                                                                          Mus musculus (Mouse)
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214 AA;
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Q9R1A5;
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RESULT
Q9R1A5
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-RACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                       GTRLEI-KRIVAAPSŲĮFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 183
                                                                                                                                                                                                                                                                                                                                                               67 APRLLIYAASNLESG#PDRFSGS--GSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQ 124
                                                                                                                 Gaps
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                                                                                                                                                                                  6 LLLVFLHHLTGSCAQLVLTQ-PSSVSTSLGSTAKLPCKA--STGNIGDSYVNWYQQYMGR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 QESVTEQDSK--DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 QGVETTQPSKQNNNKWASSYLTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234
                                                                                                                                                          7 LLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Erimates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                     Length 235;
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Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                            87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Indels
25403 MW; 39807BFE6782A3FB CRC64;
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                                                                   11;
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Pred. No. 3.9e-32;
8; Mismatches 17;
                                                                Score 428.5; DB 1
Pred. No. 6.7e-32;
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Clin. Immunol. Immunopathol. 87:184-192(1998)
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                                                                                                            36; Mismatches
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HSSP; P01789; IMCP. F
InterPro; IPR003006; FIG_MHC.
InterPro; IPR003596; FIG_V.
Pfam; PF00047; 19; 10.
SMART; SM00406; IGV; 11.
                                                                34.48;
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Best Local Similarity 75.0%;
Matches 84; Conservative E
                                                                                                              Matches 101; Conservative
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                                                                   Query Match
Best Local Similarity
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C06681716C4D16F3 CRC64;

108 AA;

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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MON-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILNE-98277139; PubMed-9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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109 AA; 11928 MW; 243325F72C7DAC83 CRC64;
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Pred. No. 4.5e-29;
9; Mismatches 21
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MEDLINE-98277139; Pubmed-9614934;
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                                                                                                                                                                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol.
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70.5%;
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HSSP; P01789; 1MCP.
InterPro; IPR003006; IQ_MHC.
InterPro; IPR003596; Ig_v.
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HSSP; P01607; 1REI.
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SMART; SM00406; 1Gv; 1.
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SMART; SM00406; IGV; 1.
NON_TER 1 1
NON_TER 108
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les 79; Conserv
                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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Matches
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STRAIN-BALB/C; Malkiel S., Zeunningham M.W., Diamond B.; Malkiel S., Liatoo L., Zeunningham M.W., Diamond B.; Maracterization offcross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
Homo sapiens (Human)
Rukaryota; Metazoa; Ébordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Frimates; Catarrhini; Hominidae; Homo.
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                                                                                                                      Gaps
                                                                                                                                                               21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0T-2001 (TrEMBLrel. 17, Last annotation update)
01-0T-2001 (TrEMBLrel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
MUS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Addentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                                                                                                                                                     81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                 Query Match 31.4%; Score 391; DB 11; Length 103; Best Local Similarity 770.6%; Pred. No. 7.1e-29; Matches 72; Conservative 16; Mismatches 14; Indels
                                                                       Length 108;
                                                                                                                      17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EC87D653DB3AAB21 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                103 AA.
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                                                                                                                   74; Conservative 17; Mismatches
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InterPro; IPR003006; Irg_MHC.
InterPro; IPR003596; Irg_NHC.
Pfam; PF00047; ig; I.
SMART; SM00406; IGV; 1.
1-1738 MW;
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                                                                     Query Match
Best Local Similarity
Matches 74; Conservi
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01-OCT-2000 (
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Q9UL79;
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                                              fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPAȚIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                 4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                     'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                    GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKR 132
                   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                              Length 108;
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                                                                                                                                                                                                                 21; Indels
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                                                                                                                                                                 DB5845F19724FB4E CRC64;
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                                                                                                                                                                                            30.9%; Score 385; DB 4;
66.1%; Pred. No. 2.7e-28;
iive 13; Mismatches 21
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09UL70;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
          PubMed=9614934;
                                                                                EMBL; AF03535; AAD56271.1; -. HSSP; P01607; 1REI. InterPro; IPR003006; Ig_MHC. InterPro; IPR003565; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. NON TER
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11787 MW;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                               74; Conservative
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                                                                                                                                                                 108 AA;
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Best Local Similarity
Matches 74; Conserv
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-070-2010 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNGGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human):
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
MAMMHALIA; Eutheria; Erimates; Catarrhini; Hominidae; Homo.
MATA TAYID-0606.
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIX-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin-reactive autoantibodies in rheumatic carditis and normal
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                         81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKR 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 381; DB 4; Length 108;
Pred. No. 6.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van dêr Merwe P.L., Kalis N.N., Berney S.M. Young D.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                       108 AA
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Q9UL85,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last sem
                                                                                                                                                                                          PRT;
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InterPro; IPR003596; iIg_v.
Pfam; PF00047; ig; 1
SMART; SM00406; IGV; 1
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Best Local Similarity 67.9%;
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HSSP; P01607; 1REI.
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                                                                                                                                                                                          PRELIMINARY;
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Clin. Immunol. Immunopathol. 87:184-192(1998).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.7%; Score 370.5; DB 4; Length 107; ilarity 63.4%; Pred. No. 5.9e-27; Conservative 19; Mismatches 17; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                    29.9%; Score 372.5; DB 4; Length 109; 67.3%; Pred. No. 3.9e-27; ive 12; Mismatches 20; Indels 5
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SEQUENCE FROM N.A.

WU X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                    109 109
109 AA: 11761 MW; FB1E43E7C7AFACCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 107
107 AA; 11501 MW; 070549FDE0754748 CRC64;
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                     EMBL; AF035029; AAD56265.1; -.
HSSP; P01607; 1REI.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003366; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM0406; IGV; 1.
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Interpro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V, Pfam; PF00047; 19; 1.
SMART; SMO0406; IGV; 1.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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nes 71; Conserv
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Q9UL81
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-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLE). 13, Created)
01-MAY-2000 (TrEMBLE). 13, Last sequence update)
01-MN-2001 (TrEMBLE). 17, Last annotation update)
MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGNENT).
Schistosoma japonicum, (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 SGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNE-DPRTFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $28.6%; Score 356; DB 4;
$59.6%; Pred. No. 1.4e-25;
£1ve 20; Mismatches 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035034; AAD56270.1; -
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Fg_v.
Pfam: PF00047; 19; 1;
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 359.6%
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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114 AA;
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=6182;
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us-09-499-662-52.rspt

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Job time: 288 sec
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Chen P. Deng J.B., Wang Z.L., Han H., Su C.Z.;
Chon P. Deng J.B., Wang Z.L., Han H., Su C.Z.;
Gens of an anti-hrnk-a monoclonal antibody.";
J. Cell. Mol. Immunol. 12:21-26(1996).
SEQUENCE FROW N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Toostruction and sequencing of the single-chain antibody gene of a human TNR-alpha specific monoclonal antibody.";
J. 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                23 VLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQAPRLLIYAASNLESGI 82
                                                                                                                                                    3 LLTQSPAIMSASPGEKVTMTCSASSSV----SYVYWYLQKPGSSPRLLIYDTSNLASGV 57
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                 5.
                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                 DB 5; Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.9%; Score 335; DB 11; Length 107; 58.9%; Pred. No. 1.1e-23; tive 17; Mismatches 25; Indels ;
                                                                                                                                                                                                                 83 PDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIK 131
                                                            Ouery Match 28.0%; Score 349.5; DB 5; Length Best Local Similarity 62.4%; Pred. No. 5.1e-25; Matches 68; Conservative 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 IPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F20F544426BAE63E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;
                                                                                                                                                                                                                                                                                                                 107 AA
                                                                                                                                                                                                                                                                                                                 PRT;
106
11478 MW;
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InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00409; IG; 1.
SMART; SM00406; IGv; 1.
NON_TER 107
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 63; Conservat
106 1
106 AA;
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NON_TER
SEQUENCE
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SEQUENCE
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Search completed: April 24, 2002, 15:13:10

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OM protein - protein search, using sw model

Run on:

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Title:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Anti-Fas humanised	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised anti-Fas	Anti-Fas humanised	Humanised anti-Fas	Humanised HFE7A de	Anti-Fas humanised	Humanised anti-Fas
SUMMARIES	AAW83033	AAB14774	AAW90924	AAW83032	AAB14773	AAW90923	AAW83035	AAB14778	AAW90928	AAW83031	AAB14772
DB	13	21	21	19	21	21	19	21	21	19	21
% Query Watch Length DB	238	238	238	238	238	238	238	238	238	238	238
% Query Match	100.0	100.0	100.0	99.1	99.1	99.1	98.6	98.6	98.6	95.6	95.6
Score	1249	1249	1249	1238	1238	1238	1231	1231	1231	1194	1194
Result No.	1	7	m	4	2	9	7	80	6	10	11

21..131 /label= Variable 132..238 /label= Constant

Protein Region Region

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This is the amino acid sequence of the MM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli sank 73697 harbors plasmid phsGwMe carrying a fusion fragment of the humanised MM type HFE7A light chain and DNA encoding the region of human kappa chain, and is deposited as FERM BP-6071 (Claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), its native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in ormal cells. The humanised antibodies are used to evaluate, in normal cells. The humanised antibodies are used to evaluate, in cormal cells. treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, and proving anamia, and also to treat syndrome, perincious anamia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
thrombopenia purpura and insulin-dependent diabetes), allergies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atopy, arterioscierosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
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                                                                                                                                                                                                                                                                                                                                                                                          Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 21; Page 202; 292pp; English.
                                  /note= "claim 9"
74..80
/label= CDR_L2
/note= "claim 9"
113..121
                                 "claim 9"
                                                                                                                                       /note= "claim 9"
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                /label= CDR_L1
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 Length 238;
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100.0%; Score 1249; DB 19;
100.0%; Pred. No. 1.2e-65;
ive 0; Mismatches 0;
                                  Conservative
                 Similarity
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 Query Match
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Glomerulonephritis, anoperation aneamia (panmyelophthisis), hepatitis AIDS and organ graft rejection. Sequences AAB14772-B14778 and AAB14777-B14778
                                                                                                                                                                                                                                                             murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; "allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand.system e.g. autoimmune diseases, contains anti-Fas antibody
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                                                                                                                                                                                                                                              antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                                                                                Humanised anti-Fas antibody light chain, SEQ ID NO:54.
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                                                                                                              Protein; 238 AA.
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Matches 238;
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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas induces apoptosis in cells with an abnormal Fas/Fas cliqand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, antialeragic, anti-arthritic, antiviral, immunosuppressive, thyromimetic, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotroptc; antinfertility; neuroprotective; antiatreriosolerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple solerosis; Basedow's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
TFCQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                    New humanized anti-Fas antibody, useful for treating or preventing e.inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                         Humanised anti-Fas antibody HFE7A light chain MM type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tamaki I, Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example reference 14; Page 119-120; 263pp; English.
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                                                                                                                                                                                                                                                                                              AAW90924 standard; Protein; 238 AA.
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N-PSDB; AAA11564.
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anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune memla, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mallitus, allergy, arteriosolerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (b, C or D) or alcoholio), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-rastantibody HEETA light chain MM type which is used in the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; slogren syndrome; perintious anaemia; Addison's disease; scleroderma; Goodpagure syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; militiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy;
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Best Local Similarity (100.0%; Pred. No. 1.2e-65;
Matches 23%; Conservative 0; Mismatches 0;
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New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                      Jun O, Kimihisa I;
Tohru T;
                                                                                                                                                      Akio S, Hideyuki H, Hiroko Y, Jı
Masahiko O, Nobufusa S, Shin Y,
                                                                                                                                                                                                                                   Claim 21; Page 200; 292pp; English
                           /note= "claim 9"
113..121
/label= CDR_L3
/note= "claim 9"
      note= "claim 9"
             74..80
/label- CDR_L2
'label - CDR_L1
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conserved in the human light (kappa) chain. Host cell E. Coli pHSGHM17 SANK 73597 harbors plasmid pHSGHM17 carrying a fusion of fragment of the humanised HM type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERW BP-6072 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematcosus, Hashimoto's disease, calsease, soleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed). This is the amino acid sequence of the HM type humanised light chain of murine anti-human Fas monoclonal antibody HFE7A. Humanisation of the murine sequence (see AAW83042) entailed making P47A and K49R amino acid substitutions; these residues are

ö Gaps ö DB 19; Length 238; Indels Score 1238; DB 19. Pred. No. 5.2e-65; 1; Mismatches 1. 99.1%; 99.2%; Best Local Similarity 99.2 Matches 236; Conservative Query Match

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QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120

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1 METDTILLWVLLLWWRRGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60

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(complementarity determining regions) to antibody HFETA. Via its interaction with Fast the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, and organ graft rejection. Sequences ABB14772-B14774 and ABB14777-B14778 represent the light chains of several humanised HFE7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                            Anti-Fas antibody, monoclonal antibody HFE7A; FERM-BP-5828, murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas Idand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains
                             qqkpgqapr111iyaasnlesg1pdrfsgsgsgtdft1t1hpveeedaatyycqqsnedpr 120
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Pred. No. 5.2e-65;
1; Mismatches 1;
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Best Local Similarity 199.28;
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Chimeric - Homo sapiens.
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Fas: antibody; human; anti-inflammatory; anti-anemic; antidabetic; antialogy; dardiantic; antivarial; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; heparotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardlomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunosmodulatory, dermatological, immunosuppressive, thyromimetic, antistremmatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                         QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                           TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                  Humanised anti-Fas antibody HFE7A light chain HM type protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example reference 14; Page 117-118; 263pp; English.
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98JP-0276882.
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diseases associated with the Fas/Fas ligand system, especially systemic lupus crythematosus. Hashimoto disease, rheumatoid arthritis, graft versus host disease. Hashimoto disease, rheumatoid arthritis, graft versus host disease, soleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, starility, myasthenia gravis, multiple sclerosis, masedow, silease, thrombopenia purpura, insulin dependent diabetes mellitus, alleray, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral CB, Cor D) or alongolic), and transplant rejection. (i) selectively inhibit apoptosis informal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in curine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human and murine disease, and have reduced risk of a humanised anti-reagantibody HEE7A light chain HM type which is used in
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chain of murine anti-human Fess monoclonal antibody HFEFA.

CHumanisation of the murine sequence (see AAM83042) entailed making DIE, P47A, K49R and R107K amino acid substitutions; these residues are conserved in the human light (kappa) chain. Host call Escherichia coli pHSHM2 SAMK 70198 harbors plasmid pHSHM2 carrying a fusion of the humanised PDHM type HFE7A light chain and DNA encoding the region of human immunoglobulin kappa chain, and is deposited as FERM BF-6272 (claimed). The invention provides choosited as FERM BF-6272 (claimed). The invention provides cells. Humanised versions of HEFA (see AAW83011-37), like native HFE7A, are capable of inducing apoptosis in abnormal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas.Fas ligand interactions, and also to treat such diseases, including autoimmune diseases that such diseases, including autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to evaluate drugs in animal models and to treat FSS-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
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                                                                                                                                                                                                                                                                                                                                                                                                                  Jun O, Kimihisa I;
Tohru T;
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S, Shin Y,
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Masahiko O, Nobufusa
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Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligang, apoptosis modulator; programmed cell death; autoimmune disease; fallergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.

Chimeric - Mus muscullus. Chimeric - Homo sapiens.

JP2000169393-A.

Humanised anti-Fas antibody light chain, SEQ ID NO:109.

24-NOV-2000 (first entry)

Protein; 238 AA.

AAB14778 standard;

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AAB14778

AAB14778;

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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFF7A, or a humanised version of HFF7A containing identical CDRs (complementarity determining regions) to antibody HFF7A. Via its interaction with Fas/F the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, anterioscierosis, myocarditis, cardiomyopathy, and anti-Fas represent the light chains of several humanised HFF7A-derived anti-Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 238;
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Pred. No. 1.3e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.68;
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Best Local Similarity
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Gaps 9

Length 238;

DB 19;

Score 1231; DB 19 Pred. No. 1.3e-64; Pred. No. 1.36 3; Mismatches

98.68; 98.38;

Conservative

Best Local Similarity Matches 234; Conserv

ò Dp

Ouery Match

METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY

g agent for the diseases caused by an abnormality system e.g. autoimmune diseases, contains

Preventive or treating the Fas/Fas ligand

N-PSDB; AAA72177.

anti-Fas antibody

99JP 0278301. 98JP-0276883.

30-SEP-1999; 30-SEP-1998;

20-JUN-2000.

(SANY) SANKYO CO LT WPI; 2000-485645/43 Claim 20; Page 103; 139pp; Japanese.

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Synthetic
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Best Local S
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                                                                                                                                                                                                                                                                                                                                         Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-res; nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple sclerosis; Basedow's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidiabetic, anti-allergic, anti-arthritic, anti-inflammatory immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antilnfertility, neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas income.
                                                                                 QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                  TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                      Gaps
                                                                                                                                                                 181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                               New humanized anti-Fas antibody, useful for treating or preventing
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example reference 21; Page 144-145; 263pp; English.
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                                                                                                                                                                                                                                                                                                                    Humanised HFE7A designed light chain protein #2.
 Mismatches
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                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                AAW90928 standard; Protein; 238
 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98JP-0276881
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                                                                                                                                                                                                                                                                                              08-AUG-2000 (first entry)
 Conservative
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Matches 234;
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antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand blading. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Slorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune Hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis ininormal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
a humanised anti-ras, antibody HEF7A designed light chain which is used in
the method described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QOKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1231; DB 21; Length 238;
Pred. No. 1.3e-64;
3; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-Fas humanised antibody HFE7A light chain HH type.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.68;
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This is the amino acid sequence of the HH type humanised light

Chain of murine anti-human Fas monoclonal antibody HFE7A.

Humanisation of the murine sequence (see AAW8304) entabled making

B47A, K49R, H80S, P81R, W8LL, E84P, E85A, A87F and T89V amino acid

Substitutions; these residues are conserved in the human light

chain (kappa chain). Host cell Escherichia coll pHSGHHT SANK 73497

harbors plasmid pHSGHH7 carrying a fusion fragment of the humanised

HH type HFE7A light chain and DNA encoding the region of human

immunoglobulin kappa chain, and is deposited as FERM BHP-6073

Claimed). The invention provides methods for producing humanised

antibodies by culturing host cells. Humanised versions of HFE7A

capanical and anormal cells expressing Fas, and of inhibiting

poptosis in abnormal cells expressing Fas, and of inhibiting

Fas-Induced apoptosis in normal cells. The humanised antibodies

care used to evaluate, in animal models, treatments of diseases that

involve Fas/Fas ligand interactions, and also to treat such

diseases, including autoimmune disease (e.g. systemic lupus

errythematowns, Hashimoto's disease, graft versus host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sjögren syndrome, pernicious anaemia, Addison's disease, scletoderma, Goodpasture syndrome, Crohn's disease, rheumatcid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, anayocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 21; Page 199-199; 292pp; English.
 label = Mat_protein
                                                                                                                                                                                           label- Variable
                                                                      label= Constant
                                                                                                                         'note= "claim 9"
                                                                                                                                                                              "claim 9"
                                                                                                                                          74..80
/label= CDR_L2
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97JP-0082953.
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                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                              (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Akio S, Hideyuki H,
Masahiko O, Nobufusa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-543440/47.
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFF7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A, via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or preferrions of the invention may therefore be used in the treatment or preferrions of conditions such as autoimmune diseases, allergy, atopy, arterioscierosis, myocarditis, cardiomyopathy, glomerulonephritis, appastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778 represent the light. Fas
                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gagent for the diseases caused by an abnormality system e.g. autoimmune diseases, contains
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                                                                                                                                                                                          tibody light chain, SEQ ID NO:50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 78-79 139pp; Japanese.
                                                                                                                                                                                                                                                                                                     AAB14772 standard; Protein; 238 AA
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in the Fas/Fas ligand
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238 AA;

Sequence

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Gaps

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Length 238; Indels

95.6%; Score 1194; DB 19; 96.2%; Pred. No. 1.8e-62; 1ive 2; Mismatches 7;

Best Local Similarity 96.2 Matches 229; Conservative

Query Match

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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                      QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQOSNEDPR 120
                                                                                                                 121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                  Gaps
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                                                                                                                                                                                                   181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY
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                                                                                                                                                                                                                                                                                                                                                       Humanised anti-Fas antibody HFE7A light chain HH type protein.
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           Length 238;
                                Indels
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        Score 1194; DB 21;
Pred. No. 1.8e-62;
2; Mismatches 7;
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                                2; Mismatches
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                                                                                                                                                                                                                                                                                   AAW90922 standard; Protein; 238 AA
        95.6%;
96.2%;
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                  Best Local Similarity 96.2
Matches 229; Conservative
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         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 238;
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Pred. No. 1.8e-62;
2; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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Best Local Similarity 196.2%;
Matches 229; Conservative
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Jun O, Kimihisa I; , Tohru T;
     /label= Sig_peptide
21..238
/label= Mat_protein
                                                                                                                                                  Hiroko Y, Ju
S, Shin Y,
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                                                               /note= "claim 9"
113..121
/label= CDR_L3
/note= "claim 9"
                         /label= Variable
                             132..238
/label= Constant
                                                 /note= "claim 9"
                                                          /label- CDR_L2
                                            /label- CDR_L1
                                                                                                           98AU-0059701.
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97JP-0169088
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                                                                                                                                                     Masahiko O, Nobufusa
                                                                                                                                        SANY ) SANKYO CO LTD
                                                                                                                                                  Hideyuki H,
                                                                                                                                                                WPI; 1998-54340/47.
                                                                                                                                                                     N-PSDB; AAV70077.
                                                                                                           30-MAR-1998;
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This is the amino acid sequence of the PDHH type humanised light chain of murine anti-human Fas monoclonal antibody HFETA.

Humanisation of the murine sequence (see AAM8042) entailed making DIE, P47A, K49R, H80S, P81R, V82L, E84P, A87F, T89V and R107K amino acid substitutions; these residues are conserved in the humanised bull kappa chain). Host cell Escherichia coli pHSHH5 SANK 70398 harbors plasmid pHSHH5 carrying a fusion fragment of the humanised PDHH type HFETA light chain and DNA encoding the reacion of human immunoglobulin kappa chain, and is deposited as FERM BP-6274 (claimed). The invention provides methods for producing humanised antibodies by culturing host encoding the reaple of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to earluste, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease, rheumatoid arthritis, autoimmune haemolytic anaemia, disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, mysathenia gravis, multiple scierosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular reference of the partitis, AIDS and transplant references. New antibodies and proteins bind conserved epitope of Fas antigen - used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis, hepatitis and AIDS rejection (all claimed).

238 AA Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-Fas antibody, monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligadi, apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AlDS; graft rejection; light chain.
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                                                                                                                                                                                                  QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                    Gaps
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                                                                                  1 METDTILLWVLLLWVRGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY
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                                    Indels
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Score 1193; DB 19;
Pred. No. 2.1e-62;
4; Mismatches 6;
                  Pred. No. 2.1e
4; Mismatches
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95.58;
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   Query Match
Best Local Similarity 95.8
Matches 228; Conservative
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Chimeric - Homo sapiens.
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                                                                                                                                                           QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
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                                                        Length 238;
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                                                      Score 1193; DB 21
Pred. No. 2.1e-62;
1; Mismatches 6
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                                                      95.5%;
95.8%;
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                                                                            Conservative
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                                                                 Similarity
                      238 AA;
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                                                                            Matches 228;
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 antibodies
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immunomodulatory, dermatological, immunosuppressive, thyromimetro, antirheumatic, nephrotropic, antinfertility, neuroprotective, antirheumatic, nephrotropic, antinfertility, neuroprotective, cardiant and hepatropic activity. (1) induce antiarteriosclerofic, cardiant and hepatropic activity. (1) induce approssis by binding to call surface Fas or inhibit it by competitive (1) diseases associated/with the Fas/Fas ligand system, especially systemic clupus erythematosus, Hashimoto disease, rehumatoid arthritis, graft versus host disease, Slorgen's syndrome, pernicious or hypoplastic commia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (8), C or D) or alcoholic), and transplant rejection. (1) selectively cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (1) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of humanised anti-Fas antibody HFFA designed light chain which is used in the method described in the invention.
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molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
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Pred. No. 2.1e-62;
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April 24, 2002, 15:10:40; Search time 42.08 Seconds (without alignments) 127.276 Million cell updates/sec
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Sequence 13, Appl
Sequence 13, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 17, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
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                                                                                                                                                              1 METDTILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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.: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-887-352B-13
US-08-466-151-9
US-09-109-207C-13
US-09-296-005-13
US-09-2855-1
US-09-054-255-1
US-08-887-352B-15
US-08-887-352B-17
US-08-887-352B-17
US-08-887-352B-19
US-09-109-207C-17
US-09-109-207C-17
US-09-109-207C-17
US-09-109-207C-19
US-09-109-207C-19
US-09-109-207C-14
US-09-109-207C-14
US-09-109-207C-14
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US-07-934-373C-25
US-08-437-642B-25
PCT-US93-07832-25
US-09-171-945-97
US-07-934-373C-39
                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-916-098A-56
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US-09-296-005-19
US-09-296-005-24
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                                                                                                                                                                                                                                   212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                   protein search, using sw model
                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 2000000000
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1249
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Perfect score:
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Sequence 39, Appl Sequence 39, Appl Sequence 5, Appl Sequence 99, Appl Sequence 10, Appl Sequence 2, Appl Sequence 2, Appl Sequence 6, Appl Sequence 6, Appl Sequence 10, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 153, Appl Se	prevention of multiple	th 218;
·	Pre-	Length
28 935 74.9 214 3 US-08-437-642B-39 29 935 74.9 214 5 PCT-US93-07832-39 30 931 74.5 235 1 US-08-157-101A-5 31 930, 74.5 214 2 US-09-171-945-99 32 930 74.5 214 2 US-09-171-945-99 34 930 74.5 214 3 US-09-097-309-2 35 930 74.5 214 3 US-09-097-309-2 36 930 74.5 214 4 US-09-097-309-2 37 930 74.5 214 4 US-09-097-171A-2 39 930 74.5 237 4 US-09-097-171A-10 40 930 74.5 237 4 US-09-097-171A-10 41 927.5 74.4 235 4 US-09-171-945-52 42 927.5 74.3 235 1 US-08-899-575-153 45 927.5 74.3 235 1 US-08-899-575-153	RESULT 1 PCT-US96-13152-2 Sequence 2. Application PC/TUS9613152 Sequence 2. Application PC/TUS9613152 GENERAL INFORMATION: JETHIE OF LINENTHAN, ULICH, et al. TITLE OF INFORMATION: ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ADDRESSEE: Felfe. Lynch ATRET: New York COUNTRY: U.S.A. COUNTRY: U.S.A. APPLICATION WHERE: PCDOS/MS-DOS SOFTWARE: ASCII CURRENT APPLICATION NUMBER: PCT/US96/13152 FILING DATE: 17-Aug-95 APPLICATION NUMBER: PC 95: 114 969.9 FILING DATE: 19-Sep-95 APPLICATION NUMBER: BOR: 1059-PCT-PFF/NDH TELECOMMUNICATION INFORMATION: NAME: Norman D. Handson REGISTERNEL/DOCKET NUMBER: BOR: 1059-PCT-PFF/NDH TELEPHONE: (212) 888-3884 INFORMATION POR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 218-383-3884 INFORMATION POR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 218-283-3884 INFORMATION POR SEQ ID NO: 2: SEQUENCE TYPE: anino acid STRANDEDNESS: single PCT-US96-13152-2	Query Match 82.5%; Score 1030; DB 5; Best Local Similarity 89.9%; Pred. No. 1.8e-76;
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organ

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121 IFPPSDEQLKSGTASYVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
                                        Score 1016; DB 3;
Pred. No. 2.5e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                         Sequence 9, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: WAIDFALIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/466163
APPLICATION NUMBER: 08/466163
FILING DATE: 15-MAR.1995
PRIOR APPLICATION DATA:
APPLICATION DATA: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA: 08/185899
PRIOR APPLICATION DATA: 08/185899
PRIOR APPLICATION DATA: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA: 07/879495
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: 99718P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/952-9681
                                                                                                                                                                                                                                                                                                                                     Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: Californ'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 88.5%;
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                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 1
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                                                                                                                                                           US-08-466-151-9
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                                                                   81 GIPDRESGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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  0; Gaps
                                    DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80
                                                        21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80
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  Indels
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  12;
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; Pred. No. 2.5e-75;
12; Mismatches 13;
                                                                                                                                                                                                                                                                          STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08887352B Patent No. 5994511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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88.5%;
Matches 196; Conservative
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Best Local Similarity 88.53
Matches 193; Conservative
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US-08-887-352B-13
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GIPDRFSGSGSGTDETLIHPVEEEDAATYYCQOSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                                                                   Gaps
                                                           21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80
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Length 218;
                               Indels
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us-09-499-662-54.rai

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81 GIPDRFSGSGSGTDETLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                           141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                                                                                    81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                                                                                                                                                                            21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
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0
                                                                                                 Length 218
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; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13
                                                                                                                                     Indels
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                                                                                           Query Match

81.3%; Score 1016; DB 4; Best Local Similarity 88.5%; Pred. No. 2.5e-75; Matches 193; Conservative 12; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                    201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.5%; Score 993; DB 4; Best Local Similarity 86.7%; Pred. No. 1.8e-73; Matches 189; Conservative 14; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Esche Ekinaduese Idusogie et al.
TITLE OF INVENTION: POLYPEPTIGE Variants
FILE REPERENCE: P1266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09282505A Patent No. 6194551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/09054255
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NAME/KEY: Artificial Sequence
LOCATION: 1-218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
US-09-282-505-1
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US-09-054-255-1
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                                                                                                                                                                                                                                                                 APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P112311
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
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CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER APPLICATION NUMBER: US 08/887,352
SEALIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 13
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                    141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Light chain sequence derived from MAE11 US-09-109-207C-13
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                                                                           STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                               181 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 218
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                                                                                                                                                                                                            Sequence 13, Application US/09109207C Patent No. 6172213
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Best Local Similarity 88.5%
Matches 193; Conservative
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                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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LENGTH: 218
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US-08-887-352B-15
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GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowertille OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                        79.5%; Score 993; DB 4; 86.7%; Pred. No. 1.8e-73; iive 14; Mismatches 15
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           GENERAL INFORMATION:
APPLICANT: Esohe Ekinaduese Idusogie et al.
TITLE OF INVENTION: Polypeptide Variants
FILE REFERENCE: P1266
CURRENT APPLICATION NUMBER: US/09/054,255
CURRENT APPLICATION DIS: 1998-04-02
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Uul-1997
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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STATE: California
COUNTRY: USA
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,0
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Best Local Similarity 86.7
Matches 189; Conservative
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US-08-887-352B-15
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
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                                                                                   79.3%; Score 990; DB 2; L. 86.2%; Pred. No. 3.2e-73; Live 15; Mismatches 15;
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79.3%; Score 990; DB 2;
Best Local Similarity 86.2%; Pred. No. 3.2e-73;
Matches 188; Conservative 15; Mismatches 15
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
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FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
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Patent No. 5994511
GENERAL INFORMATION:
APPLICANT: HENRY B. Lowman, Leonar
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CURRENT APPLICATION DATA:
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NAME: SYODOGA, CEALG G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: PI.
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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Amino Acid
                                                                                      Query Match
Best Local Similarity 86.29
Matches 188; Conservative
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TOPOLOGY: Linear
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Matches 188;
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NUMBER OF SEQUENCES: 26
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              GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.3%; Score 990; DB 2; Length 218; 86.2%; Pred. No. 3.2e-73; 1ive 15; Mismatches 15; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                  Sequence 19, Application US/08887352B Patent No. 5994511 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
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NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,04
REFERENCE/DOCKET NUMBER: P1123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DO: SOFTWARE: WinPatin (Genentech)
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STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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LENGTH: 218 amino acids
TYPE: Amino Acid
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Best Local Similarity 86.2%,
Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
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US-08-887-352B-19
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Sequence 15, Application US/09109207C

Batent No. 6172213

GENERAL INFORMATION:

TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
FILE REFERENCE: P1123H

CURRENT APPLICATION NUMBER: US/09/109,207C

CURRENT FILING DATE: 01998-06-30
Sequence 24, Application US/08887352B

Patent No. 5994511
GRNERAL INFORMATION:

APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improving Polypeptides

TITLE OF INVENTION: Improving Polypeptides

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA WAY

CITY: South San Francisco

STREET: 1 DNA MAY

CITY: South San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   In 79.3%; Score 990; DB 2; Length 218; Similarity 86.2%; Pred. No. 3.2e-73;
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                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC.COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 218 amino acids
Amino Acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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US-08-887-352B-24
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    US-08-887-352B-24
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypept FILE REFERENCE: P1123R1 CURRENT APPLICATION NUMBER: US/09/109,207C CURRENT APPLICATION NUMBER: US/09/109,207C PRIOR APPLICATION NUMBER: US 60/051,554 PRIOR APPLICATION NUMBER: US 60/051,554 NUMBER OF SEQ ID NOS: 1997-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypept;
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109, 207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
          121 IFPPSDEQLKSGTASWVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DIVLTQSPGTLSLSBGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11 US-09-109-207C-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 990; DB 4;
; Pred. No. 3.2e-73;
15; Mismatches 15
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                                                                        181 STLTLSKADYEKHKWYACEVTHQGLSSPVTKSFNRGEC
                                                   201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                        US-09-109-207C-19; Sequence 19, Application US/09109207C; Patent No. 6172213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 24, Application US/09109207C; Patent No. 6172213
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Best Local Similarity 86.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Artificial
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US-09-109-207C-24
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LENGTH: 218
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109, 207C
CURRENT FILING DATE: 1998-06-30
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
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                                                                                                                                                                                                                                                                                         79.3%; Score 990; DB 4; Length 218; 86.2%; Pred. No. 3.2e-73; 1.1ve 15; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 218;
                                                                                                                                                                                                        ; OTHER INFORMATION: Light chain sequence derived from MAE11 US-09-109-207C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-17
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86.2%; Pred. No. 3.2e-73;
iive 15; Mismatches 15
      US 60/051,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/09109207C Patent No. 6172213
PRIOR APPLICATION NUMBER: US 60
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 15
LENGH: 218
TYPE: PRT
ORGANISM: Artificial
FRAUGNE:
NAME/KEY: Artificial
LOCATION: 1-218
                                                                                                                                                                                                                                                                                                              Best Local Similarity ov.
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Matches 188; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-109-207C-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 17
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Best Local 8
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US-09-109-207C-24
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79.3%; Score 990; DB 4; Length 218; 86.2%; Pred. No. 3.2e-73;	Matches 188; Conservative 15; Mismatches 15; Indels 0; Gaps 0;	21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQRPGQPPKLLIYAASNLES 80	1 DIQLIQSESSLSASVGDRVIITCRASKPVDGEGDSYLNWYQQKPGKAPKLLIYAASYLES 60	81 GIPDRESGSGSGTDFTLITHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140	61 GVPSRFSGSGSGTDFTLTISSLQPEDFATYZCQQSHEDPYTFGGGTKVEIKRTVAAPSVF 120	141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200	IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180	201 STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238	
Query Match Best Local Similarity 86,2%	188; Conservative	DIVLTQSPGTLSLSPGERATI	DIQLTQSPSSLSASVGDRVTI	GIPDRESGSGSGTDFTLTIHE	GVPSRFSGSGSGTDFTLTISS	IFPPSDEQLKSGTASVVCLLN	IFPPSDEQLKSGTASVVCLLN	STLTLSKADYEKHKVYACEVI	STLTLSKADYEKHKVYACEVT
Query Match Best Local	datches	21	1	81	61	141	121	201	181
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Search completed: April 24, 2002, 15:10:41 Job time: 144 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

Run on: April 24, 2002, 15:11:37 ; Search time 49.97 Seconds

(without alignments)
362.809 Million cell updates/sec
ng-ng-409-662-54

Title: US-09-499-662-54

Perfect score: 1249
Sequence: 1 METDTILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
Scoring table: BLOSUM62 Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum' Match 0% Maximum Match 100% Listing first 45 summaries

Listing first 4
Database : PIR_68:*

ase: PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Iq kappa chain NIG		kappa chain	chain	kappa chain		kappa chain		Ig kappa chain V r		kappa	kappa chain	kappa chain (m			kappa chain -	kappa chain -	chain -				kappa chain	kappa chain	kappa chain	kappa chain	-kappa protei	kappa	Ig lambda-like cha	Ig kappa chain pre
SUMMARIES	ID	JE0242	JE0244	JE0243	A23746	JE0241	S06084	S68241	JC5810	A56169	A31790	S14237	S33161	PC4203	S52028	S37484	S38865	S25058	S42772	S16112	S68212	S01320	JL0029	PH1226	PT0219	S29593	S52059	A20969	A49633	KVMSM6
	DB	2	~	~	~	7	~	7	7	7	7	~	7	7	7	7	7	7	~	~	~	~	~	7	7	7	7	7	7	٦
	Length	215	215	215	215	216	240	218	218	210	220	234	230	219	219	225	219	235	217	219	214	234	225	131	178	197	135	229	238	131
ф	Query Match	.76.7	73.6	71.6	71.5	70.5	ë.	63.0	62.9	61.6	58.3	57.2	56.9	26.7	56.5	56.3	56.2	56.1	55.4	55.4	55.1	54.8	54.1	50.1	49.8	48.4	48.2	48.2	45.4	44.8
	Score	958.5	919.5	894.5	892.5	881	196	787	785	770	728	714	710.5	708.5	705.5	703.5	701.5	700.5	692.5	692.5	688	684	675.5	626	622	604.5		02.	566.5	10
	Result No.	1	7	٣	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

C. Species: Homo sapiens (man)
C. Date: 05-Dec-1998 #text_change 21-Jan-2000
C. Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C. Accession: JE0044
R. Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, submitted to JIPID. November 1998
A. Description: A new subgroup of k type light chains (VkV) identified in cases of AI
A. Reference number: JE0043

A; Accession: JE0244
A; Molecule type: protein
A; Residues: 1-715 < ALL>
C; Superfamily: immunoglobulin V region; immunoglobulin homology

chain (chain	light chain	kappa chain	kappa chain	kappa chain	kappa chain	kappa chain	Ig kappa chain V r	kappa chain	kappa	kappa	light chain	kappa	kappa	kappa	
кзни	PN0446	\$55027	PL0106	KVMS32	KVMS43	KVMS83	KVMS08	S19971	KVMS69	S20631	A37927	529577	S26653	KVMS10	KVMSC1	
106 1	.140 2	131 2	144 2	7132 1	: 111 1	\$111 1	1111 1	1112 2	111 1	145 2	99 2	.233 2	. 99	110 1	1111 1	4
43.9	43.8	43.6	43.3	43.2	42.3	42.1	42.0	41.9	41.7	41.6	41.1	40.8	40.6	40.3	40.3	
548	547	544	541	540	528	526	524	523	521	519.5	513	509	507	503.5	503	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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g kappa chain NIG26 precursor - human class (man) (class Homo sapiens (man) (class Homo sapiens (man) (class Homo sapiens (man) (class in the color) 198 #text_change 21-Jan-2000 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0242 (classion: JE0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.8%; Pred. No. 2e-55;
Matches 187; Conservative 11; Mismatches
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Query Match
Best Local Similarity
Matches 181; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.; Kazi,
                                                                                                                                                                                                                                                                                                                                                                                                                  Gyappa chain NIG93 precursor - human cyspecies: Homo sapiens (man) cyspecies: Homo sapiens (man) cyspecies: Homo sapiens (man) cyspecies: Homo sapiens (man) cyspecies: Homo sapiens (man) cyspecies: Homo sapiens (man) sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 (Cyspecision: JE0243 Ryalim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, submitted to JIPID, November 1998 A; Reference number: JE0243 A; Reference number: JE0243 A; Reference number: JE0243 A; Reference number: JE0243 A; Residues: 1-215 <ALI>C; Superfamily: Immunoglobulin V region; immunoglobulin homology <IMM>
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                                                                                                                                                                                              GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNE-DPRTFGQGTRLEIKRTVAAPSV 139
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                                                                                                                               DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
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19 kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Ja:
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Ja:
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Ja:
S;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Telerier primary structure of the Fab fragment of protein KAU, a s;Reference number: A23746; MUID:91131575
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                                                  Length 215;
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                                                                                21;
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80.8%; Pred. No. 2.8e-51;
ive 15; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                           Score 919.5; DB 2 Pred. No. 6.7e-53;
                                    73.6%; Scc. 83.1%; Pred. No. o.. 43.1%; Pred. 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 71.67
Best Local Similarity 80.8°
Matches 177; Conservative
                                                               Best Local Similarity 83.1
Matches 182; Conservative
                                                  Query Match
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C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Species: Homo sapiens (man)
C. Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C. Accession: JED241
R. Alim, M. A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIPID, November 1998
A. Pescription: Structure relationship of kappatype light chains with AL amyloidosis: A. Reference number: JED241
A. Recession: JED241
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                                                                                                                                                                                                                                                                                                                                                                                           GIPDRFSGSGSGTDFTLTHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                                                                                                                                                        215;
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change
C;Accession: S06084 **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 1-216 <ALIS-
C: Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                      Length
                                                                                                                                                                                                                  Indels
                                                 immunoglobulin
                                                                                                                                                                 Score 892.5; DB 2;
Pred. No. 3.7e-51;
9; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
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Pred. No. 2.1e-50;
5; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STLTLSKADYEKHKWYACEVTHQGLSSPVTKSFNRGE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC
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A,Molecule type: protein.
A,Residues: 1-215 <LEO>
C,Superfamily: immunoglobulin V region; immuno C,Reywords: heterotetramer; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15;
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nilarity 83.4%;
Conservative 9
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Best Local Similarity 80.3%;
Matches 175; Conservative 15
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24 15:21:26 2002

Wed Apr

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C;Accession: JC5810
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a por A;Reference number: JC5810; MuID:98063277
A;Accession: JC5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Molecule type: protein.
A.Residues: 1-218 <a href="Acktack">A.Residues: 1-218 <a href="Acktack">A.Residues: 11-218 <a href="Acktack">A.Residues: 11-218 <a href="Acktack">Acktack</a>
C.Comment: This catalytic antibody has peroxidase oxidase. It is directed against a C.Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     If Kappa chain V region (clone 23.2) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C; Accession: A56169
B; Monfardini, C.; Kleber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum J. Biol. Chem. 270, 6628-6638, 1995
A; Title: Recombinant antibodies in bioactive peptide design.
A; Reference number: A56169; MUID:95204454
A; Actus: preliminary; not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-210 < AONN>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 04-Feb.1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
               GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
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                                                                                                                                                                                                                         Query Match (62.9%; Score 785; DB 2; Best Local Similarity 67.4%; Pred. No. 3.4e-44; Matches 147; Conservative 27; Mismatches 44.
                                                                                                                                                                                         STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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69.4%; Pred. No. 3e-43;
11ve 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         monoclonal antibody 13-1 light chain - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 69.4
Matches 145; Conservative
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                                                                                          141
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R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

Nucleic Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain CDNP A; Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain CDNP A; Reference number: S06084; MUID:90016888

A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-240 <CRO>A; Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Superfamily: immunoglobulin y region; immunoglobulin homology
F; 1-20/Domain: signal sequence #status predicted <NIC>F; 1-20/Domain: immunoglobulin homology <NMM>
F; 153-222/Domain: immunoglobulin homology <NMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V region (Mabl3-1) - mouse (fragment)

Na Alternate names: immunoglobulin light chain

C; Species: Mus musculus (house mouse)

C; Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C; Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C; Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

R; Accession: S68241

S; Description: Specific paroxidase activity by formation of an antibody L-chain-porphyrians A; Reference number: S68241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin A/Reference number: $68211; MUID:96085223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-218 <TAK>
A;Cross-references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
R;Tekagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,
FEBS Lett. 375, 273-276, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 WYQQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNED 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 PRIFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 QSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 787; DB 2; L
Pred. No. 2.5e-44;
); Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 796; DB 2;
Pred. No. 7.3e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.0%; Sconilarity 67.0%; Pre
Conservative 29;
                                                                                                                                                                                                                                                                                                                                                                                              63.78;
62.98;
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C;Superfamily: immunoglobulin V )
C;Keywords: immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 'NI', 3-212 <TAW>
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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A;Status: nucleic ac
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Sim
Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Best Local
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B.; Rosenbaum, H.; G⊂

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Gaps

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Indels Length

26

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Ig kappa chain (monoclonal antibody MabA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
R;KwaK, J W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: 533161
R; Foley, R.C.; Beh, K.J.
submitted to the EMBL Data Library, July 1990
A; Description: Isolation and characterisation of sheep kappa light chain CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin c;Reywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                    121 TFGQGTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
                                                                                                                                                                                                                               61 QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                              1 METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                                     OPPKLLIYAASNLESGIPDRESGSGSGTDFTLTIHPVEEBDAATYXCQSNEDPRTFGGG
                                                                                                                                                                       7 LLWVLLLW-VPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE
                                                                                                                                                                                                                                                                                                                                                                                                                   181 GNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.9%; Score 710.5; DB 2; 58.4%; Pred. No. 2.4e-39; ive 37; Mismatches 55;
                                                                                                        64;
                                                             ; DB 2;
1.4e-39;
                                                                                                          Mismatches
    F;36-110/Domain: immunoglobulin homology <IMM>
                                                             Score 714;
Pred. No. 1.
                                                                                                      35;
                                                           Query Match
Best Local Similarity 56.7%;
Matches 135; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S33161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S33161
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-230 <FOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 136; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain - sheep
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: S14237
C; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur, J. Blochem. 192, 767-775, 1990
A; File: Construction and characterization of a recombinant murine monoclonal antibody A; Reference number: S14237
A; Mccession: S14237
A; Mcloule type: mRNA
A; Residues: 1-234 <VANA.
A; Residues: 1-234 <VANA.
A; Cross-references: EMBL:X56394; NID:951622; PIDN:CAA39805.1; PID:951623
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.H.; Wilson, I.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:AAA39162.1; PID:9533235
homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                                                                                                                                 Targets: Ms musculus (house mouse)
C; Species: Ms musculus (house mouse)
C; Species: Ms musculus (house mouse)
C; Species: Ms musculus (house mouse)
C; Accession: A31790
C; Accession: A31790
C; Accession: Chem. 263, 171100-17105; 1988
A; Title: Preliminary crystallographic data, primary sequence, and binding data is A; Reference number: A92686; MUID:89034213
A; Accession: A31790
A; Accession: A31790
A; Accession: A31790
A; Residues: 1-220 csCH>
A; Residues: 1-220 csCH>
C; Superfemences: GB:V3606; GB:V4061; NID:5533234; PIDN:AAA39162.1; PID:953:C; Superfemences: heteroctetramer; immunoglobulin
F; 16-96/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                   200
                                                                                GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                                      ESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIVLTQSPGTLSLSPGERATLSCKASQSVDYDG--DSYMNWYQQKPGQPPKLLIYAASNL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
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R. Van Engelen, F.: Schouten, A.: Molthoff, J.W.; Roosien, J.: Dirkse, W.G.; Schots, A.; submitted to the EMBL Data Library, August 1994
A.Description: Coordinate expression of antibody subunit genes yields high levels of fun A; Reference number: 552028
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C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
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A; Title: Cloning and characterization of A; Reference number: PC4202; MJID:97082978
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Matches 132; Conservative
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1g kappa chain - mouse (fragment)
1g kappa chain - mouse (fragment)
2; Species: Mus musculus (house mouse)
2; Species: Mous musculus (house mouse)
2; Species: 06-7an-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
2; Accession: S37484
R; Ducancel, F.F.D.
37, Reference number: S37483
                                                                                                                                                                                                                                                                                                                              A.Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 60.5%
Matches 138; Conservative
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-225 <DUC>
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Page 1

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April 24, 2002, 15:13:45; Search time 29.21 Seconds (without alignments) 298.741 Million cell updates/sec
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1 METDTILLWVLLLWVPGSTG......EVTHQGLSSPVTKSFNRGEC 238
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P01661 mus musculu	P01834 homo sapien	в mus ш	5 mus	P01666 mus musculu	P01667 mus musculu	P01669 mus musculu	8 mus	P01664 mus musculu		P18136 homo sapien	mus m	gnw 0		2 mus	3 mus	mus m	homo	7 homo	4 homo	3 mus m	P01656 mus musculu	Snm 6	4 mus m	P06313 homo sapien	mus m	P03977 mus musculu	0 homo	^	P01622 homo sapien	131 homo	310 homo	PO4433 homo sapien
SUMMARIES	ID	m	KAC_HUMAN	KV3F_MOUSE	KV3M_MOUSE	KV3N_MOUSE	KV30_MOUSE	KV3Q_MOUSE	KV3P_MOUSE	KV3L_MOUSE	KV3L_HUMAN	KV3M_HUMAN	KV3R_MOUSE	KV3H_MOUSE	KV3S_MOUSE	KV3J_MOUSE	KV3K_MOUSE	KV3T_MOUSE	KV3K_HUMAN	KV3H_HUMAN	KV4C_HUMAN	KV3U_MOUSE	KV3C_MOUSE	KV3G_MOUSE	KV3A_MOUSE	KV4B_HUMAN	KV3B_MOUSE	KV3D_MOUSE	KV3B_HUMAN	- 1	KV3D_HUMAN	KV1W_HUMAN	KV2F_HUMAN	KV3I_HUMAN
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Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Mule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappar-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
                                                                                                  QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                 Gaps
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                                       METDTILLWVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
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Hieter P.A., Max E.E., Seidman J.G., Malzel J.V. Jr., Leder P.;
Hieter P.A., max E.E., Seidman J.G., Malzel J.V. Jr., Leder P.;
Cloned human and mouse Kappa immunoglobulin constant and J region
genes conserve homology in functional segments.";
Cell 22:197-207(1980).
                                                  SEQUENCE (BENCE-JONES PROTEIN ROY).
Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
Fatinmetz-Kayne M., Suter L., Watanabe S.;
(In) Franck F., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press,
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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   Pred. No. 8.3e-39;
5; Mismatches 11;
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21-JUL-1986 (Rel. 01, Last sequence update)
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MEDLINE=71064027; PubMed=4923144;
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MEDLINE-71064023; Pubmed-5489770;
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Biochemistry 9:3188-3196(1970).
               104; Conservative
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This SWISS-PROT enery is copyright. It is produced through a collaboration between the Swiss-firstitute of Bioinformatics and the BBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this Statement is not removed. Usage by and for commercial entities requires allicense agreement (See http://www.isb-sib.ch/announce/or send an email tollicense@isb-sib.ch).
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SEQUENCE (BENCE-JONES PROTEIN AG).
MEDLINE-69234734; Purded-4893682;
Titani K., Shinodarg, Putnam F.W.;
The amino acid seguence of a kappa type Bence-Jones protein, 3. The complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 24403550-3560(1969).
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-!- MISCELLANEOUS:THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER, 45-ALA & 83-VAL THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC MARKER, 45-ALA AND 83-LEU.
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15-JUL-1996 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 28, Last annotation update)
16 KAPPA CHAIN V-LTG REGION MOPC 321 PRECURSOR.
Mus musculus (Munus 6).
Eukaryota: Metazoa 6).
Monmalia: Butherias Rodentia; Sciurognathi; Muridae; Musinae; Mus
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A., Paul C., Putnam F.W.;
cture: variable sequence of light and heavy
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Pred. No. 4.9e-38;
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-!- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
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MEDLINE=73140224; PubMed=4120629;
MCKean D.J., Potter M., Hood L.E.;
"Mousee immunoglobulin chains. Partial amino acid sequence of a kappa chain.";
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        Burstein Y., Schechter I., "Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes."; Biochemistry 17:2392-2400(1978).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMART: SM00406; IGv; 1.
Immunoglobulin V region; Bence-Jones protein; Signal.
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1G KAPPA CHAIN V-III REGION PC 7043.
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MEDLINE-78235887; PubMed-98179;
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88.3%;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Nature 276:785-790(1978).
PIR; A01937; KVMS43.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Best Local Similarity 89.29
Matches 99, Conseryative
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                                                        Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region
DOMAIN
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SMART; SM00406; IGV; 1.
Immunoglobulin V region
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Best Local Similarity
Matches 98; Conserva
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MEDLINE=79073152; PubMed=103003;
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P01668;
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KV3P_MOUSE
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                   1 DIVLIQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-79073152; PubMed-103003;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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COMPLEMENTARITY-DETERMINING
FRAMEWORK 4.
BY SIMILARITY.
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42.0%; Score 524; DB 1; Length 11
Best Local Similarity 88.3%; Pred. No. 4.6e-36;
Matches 98; Conservative 6; Mismatches 7; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-ADPA CHAIN V-III REGION PC 7769.
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PIR; C01937; KVMSO8.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam: PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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P01669;
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P01667;
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KV3O_MOUSE
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 03, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G KAPPA CHAIN V-IFF REGION PC 7210.
Mus musculus (Mouse)
Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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Pred. No. 8.1e-36;
8; Mismatches 6; Indels
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BY SIMILARITY.
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SEQUENCE.
MEDLINE=79073152; PubMed=103003;
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Nature 276:785-790(1978).
PIR; D01937; KWMS10.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR00396; Ig_V.
Pfam; PF00047; 1g; I.
SMART; SM00406; IGV; I.
                                  Alture 276:785-790(1978).
PIR, E01937; KVMS69.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003306; Ig_V.
Pfam; PF00047; ig; 'l.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
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Best Local Similarity 87.4%;
Matches 97; Conservative
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121 TFGQGTRLEIKR 1132
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P18136;
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Matches
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MCKean D.J., Bell M., Potter M.;
MCKean D.J., Bell M., Potter M.;
Mackanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
-i - MISCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN.
INTERPRO: JPR003006; Ig_AMC.
InterPro: IRR003596; Ig_V.
SMART; SM00406; Ig; 1.
SMART; SM00406; IGv; 1.
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                                           DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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        Length 110;
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Pred. No. 2.3e-34;
7; Mismatches 9; Indels
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Score 503.5; DB 1;
Pred. No. 2.1e-34;
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION CBPC 101.
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 APPA CHAIN V-III REGION HAH PRECURSOR.
HOMO sapiens (Human).
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85.6%;
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P18135;
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SEQUENCE
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KV3L_MOUSE
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1 METDTILLEWVLLEWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1999 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 16, Last sequence update)
16 KAPPA CHAIN V-161 REGION HIC PRECURSOR.
HOMO Saplens (Human).
Eukaryota; Metazoan Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherian Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoan Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KAPPA CHAIN V-III REGION HAH.
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FRAMEWORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMEWORK 2.
COMPLEMENTARITY-DETERMINING 2.
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JEASE: THE PROTE.

AUTOANTIBOIES EXPR.

JM PIR; PLO02; KHUHAN.

DR HSSP, P01789; ZMCP.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR00396; Ig_W.

DR SMART; SM00406; IGV; I.

Wannuncylobulin V region; Signal.

SIGNAL 1 20 IG KAPPA Ct.

CHAIN 21 43 FRAMEWORK 1.

VAIN 44 55 COMPLEMENTARITY-D.

TO 77 COMPLEMENTARITY-D.

TO 77 COMPLEMENTARITY-D.

TO 77 COMPLEMENTARITY-DF.

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                                                                                                                                                                                                                                                                       61 QQKPGQPPKLLIYAASNLESGIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                   AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                   DB 1; Length 129;
                                                                                     KAPPA CHAIN V-III REGION HIC.
                                                                                    IG KAPPA CHAIN V-III REGION HIC
FRAMENORK 1.
COMPLEMENTARITY-DETERMINING 1.
FRAMENORK 2.
COMPLEMENTARITY-DETERMINING 2.
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                                                                                                                                                                         7395528EA2BB74D6 CRC64;
                                                                                                                                                                                                 38.4%; Score 479.5; DB 1; 71.2%; Pred. No. 2.3e-32; tive 13; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel..01, Created)
21-JUL-1986 (Rel..01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-RAPPA CHAIN V-III REGION PC 6684.
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               PIR; PLO021; K3HUHI.
HSSP; P01789; 2MCP.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
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InterPro, IPR003006, Ig_MHC.
InterPro, IPR003596, Ig_V.
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| 118 TFGQGTKVEIKR 129
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129 AA;
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Best Local Similarity
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ID KV3R_MOUSE
AC P01670;
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MEDELINE=79012520; Rubmed=99744;
McKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S. 75:3913-3917(1978).
-1- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
                                                                                                                   Gaps
                                                                                                                                                                                                 9
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P01660;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 KAPPA CHAIN V-III REGION PC 3741/TEPC 111.
Mus musculus (Mouse).
Bukaryota; Metazoa Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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SEQUENCE (PC 3741).

Medigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;

Wearrangement of agenetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                     61 GVPARFSGSGSGTOFTLNIHPWEEEDAATYYCOHSRELPRTFGGGTKLEIK 111
                                                                                                                                                                                                                                        TLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GIPARFSGSGSKIDETLIINPVEADDVATYYCQQSNEDPYTFGGGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 GIPDRFSGSGSGTØFTLTIHPVEEEDAATYYCOOSNEDPRTFGGGTRLEIK 131
                                                                         Length 111;
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InterPro; 1.

InterPro; 1.

InterPro; 1.

Pfam; PF00047; 1g;

Pfam; PF00047; 1g;

NM Immunoglobulin V region.

FT DOMAIN 1 23 COh.

FT DOMAIN 39 53 FRAMEW.

FT DOMAIN 54 60 COMPLEMENT.

NOMAIN 61 93 101 COMPLEMENT.

102 111 FRAMEWORK 3.

112 92 BY SIMILARITY.

111 SCORE 461; DB 1; Length

"d. No. 5.9e-31;

"matches 11; T
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.11
12039 MW; 1E46988341858526 CRC64;
                                                                         37.2%; Score 465; DB 1; 79.3%; Pred. No. 2.8e-31;
                                                                                                                 10; Mismatches
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-!- MISCELLANEOUS: THE PC 374
PIR; A01934; KWMS3,
InterPro; IPR003006; I9_MHC.
InterPro; IPR003596; I9_V.
                                                                     Query Match
Best Local Similarity 79.39
Matches 88; Conseivative
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111 AA;
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McKean D.J., Bell M., Potter M.;
Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
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                                                                                                                                                                             Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.6%; Score 457; DB 1; Length 111; 77.5%; Pred. No. 1.2e-30; Live 11; Mismatches 14; Indels
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COMPLEMENTARITY-DETERMINING
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21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.
                                                         21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG KAPPA CHAIN V-III REGION PC 7175.
                        111 AA
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                       PRT;
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MEDLINE=79073152; Pubmed=103003;
                                              01, Created)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Matches 86; Conservative
                                                                                                                                                                                                               Nature 276:785-790(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                       STANDARD;
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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                                                                                            Mus musculus (Mouse)
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SEQUENCE (PC 9245)
                                               (Rel.
                                              21-JUL-1986
                   KV3S_MOUSE
P01671;
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P01662;
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           KV3S_MOUSE
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Gaps
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Nature 276;785-790(1978).
Nature 276;785-790(1978).
InterPro: BROUGHER ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
PIR; A01935; KYMSM6.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
SMART; SM00406; IGY; 1.
Immunoglobulin V region.
         Weigert M., Garmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
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                                                                                                                                                                                                                                                                      12041 MW; D7DF0609303453CE CRC64;
                                                                                                                                                                                                                                                                                                            36.3%; Score 454; DB 1; 76.6%; Pred. No. 2.2e-30; Live 15; Mismatches 11,
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MEDLINE=79073152; PubMed=103003;
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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Sequence:
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                                                                    OM protein
                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_vertebrate:*

sp_virus:*

sp_organelle:* sp_phage:*

sp_mammal:* sp_mhc:*

sp_plant:* sp_rodent:*

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_lnvertebrate:*

SUMMARIES		Description	O99m37 musculu	09r1a5 mus	099m11 mus	09ul78 homo	mus	ОШО	Omo	Omo	ОШО	ОШО	ОШО		Omo	chis	Q9erz9 mus musculu	mus	091178 mus musculo	091176 mus	091182 mus
SOM		ΩI	099M37	09R1A5	099M11	Q9UL78	09JL80	Q9UL77	OSUL86	Q9UL70	Q9UL79	Q9UL83	Q9UL81	Q9UL85	Q9UL80	090410	Q9ERZ9	Q9JL74	Q9JL78	99JL76	Q9JL82
		DB	: #	11	11	4	11	4	4	4	4	4	4	4	4	5	11	11	11	1	11
		Query Match Length DB	238	214	235	109	103	108	109	108	108	108	107	109	114	106	107	66	101	97	104
	ф	Query Match	59.7	54.5	34.1	33.5	32.2	31.0	30.9	30.7	30.5	29.9	29.3	29.5	28.1	27.6	26.7	26.4	26.3	26.3	25.8
		Score	745.5	681	426.5	418.5	402	387	385.5	384	381	373	365.5	364.5	351	344.5	334	330	329	328	322.5
		Result No.	-	2	m	4	Ŋ	9	7	∞	6	10	11	12	13	14	15	16	17	18	19

GTRLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 184

125 125

9

D δ QQ 185

185

δ Dp

11 090YF0 099yf0 mus musculu 091L84 mus musculu 091L84 0910NW5 091C003 0910NW5 091DW5 091DW5 0Y0NW5 0Y0NM5	PRT; 238 AA. Treated) Last sequence update) Last annotation update) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. FB2B06A0B801330A CRC64; Score 745.5; DB 11; Length 238; Pred. No. 2.4e-61; Mismatches 56; Indels 1; Ga	ILLMVLLLWVPGSTGDIVLTQSPGTLSLSPGERATLSCKASQSVDY-DGDSYMNWYQQKP 64 **I
20 319 25.5 298 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	SULT 1 09M37 099M3 0999M3 091-JU 01-JU 01-	Oy 6 ILLWVLLLWVPGSTGDIVLTO

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39807BFE6782A3FB CRC64;
235 AA; 25403 MW;
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11646 MW;
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                                  Query Match
Best Local Similarity 42.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01789; IMCP;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1
                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBEREL: 13, 01-JUN-2001 (TrEMBEREL: 17,
                                                        Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82; Conservative
                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00406; 19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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SEQUENCE
  SEOUENCE
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Q9JL80
ID Q9J
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Q9UL78
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                               Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.,;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKRTVAAPSVF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                54.5%; Score 681; DB 11; Length 214; 58.7%; Pred. No. 2e-55; 11ve 32; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC002129; AAH02129.1; -.
                                                                                                                                                                                                                                                                                                                                                                                  52BA205FDE995E2A CRC64;
                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) UNKNOWN (PROTEIN FOR MGC:6743).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 AA
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                                                                                                                                                                                                                                               EMBL, AFI52371; AAD40242.1; -... HSSP: P01789; 1MCP.
InterPro: IPR003600; Ig_like.
InterPro: IPR003600; Ig_MC.
InterPro: IPR03596; Ig_V.
Ffam: PF00047; 1g; 2.
SMART; SM00406; IGV: 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seq
                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                      214 214
214 AA; 23922 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 58.79
Matches 128; Conservative
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                            Mus musculus (Mouse)
                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                NCBI_TaxID=10090;
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NON_TER
SEQUENCE
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                                   Q9R1A5;
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                       09R1A5
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RESULT
09R1A5
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Q99M11
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MYOSIN-REACTIVE INMUNOCLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).

Homo saplens (Human).

Eukaryota; Metazoan Chordata; Craniata; Vertebrata; Euteleostomi;

Mammaliai, Eutherian Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: TOWNINGCLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                          63 SPINMIYGDDLREGGSPSPRFSGSIDSSSNSAFLTIQNVQADDEADYYCQSYSSGIRVFGG 122
                                                                                                                                                                                                                                                                                                 123 GTKLTVLSQPKTSBSVTLFPPSSEELETNKATLVCTISDFYPGVVTVDWKADG---TPVT 179
                                                                                                                                                                                                                                                                                   67 PPKLLIYAASNLESGIPDRFSGS--GSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQ 124
                                                                                                            Gaps
                                                  Gaps
                                                                                           7 LLMVLLLWVPGSRĞDIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 QESVTEQDSK--DSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
                                                                                                                                                                                                                                                                                                                                                                                                  180 QGVETTQPSKQNWYXMASSYLTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                13;
Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQOSNEDPRTFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 418.5; DB 4; Length 109;
Pred. No. 1.9e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.*
SEDCINCE FROM N.A.*
SEDCINE-98277139; Bubmed-9614934;
Wu X., Liu B., Vanader Merwe P.L., Kalis N.N., Berney S.M.,
Wu X., Liu B., Vanader Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                  88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5F675C52EC7EE197 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
    DB 11;
  Score 426.5; DB 1
Pred, No. 9.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA.
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                                                  35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103
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NON_TER
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SEQUENCE
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                                                                                                          81
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                                                                                                                                                                    RESULT
Q9UL86
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                                                                                                                            Malkiel S., Lido L., Cunningham M.W., Diamond B.;
Malkiel S., Lido L., Cunningham M.W., Diamond B.;
Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                      30 TLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPDRFSGS 89
                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
           01-OCT-2000 (TIEMBLRel. 15, Created)
01-OCT-2000 (TIEMBLRel. 15, Last sequence update)
01-UNY-2001 (TIEMBLRel. 17, Last annotation update)
ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                .;
0
                                                                                                                                                                                                                                                                                                                                      32.2%; Score 402; DB 11; Length 103; 72.5%; Pred. No. 6.1e-30; ive 15; Mismatches 13; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                        103 103
103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11738 MW; C06681716C4D16F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA.
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SEQUENCE FROM N.A.
MEDLINE=98277139; Pubmed=9614934;
                                                                                                                                                                                                               EMBL; AF206026; AAF69324.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF035037; AAD56273.1; HSSP; P01607; IREI. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                SM00406; IGv; 1.
                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1. SMART; SM00406: TEV: 1
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108 AA;
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 74; Conserv
                                                                                                                  SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=10090;
          01-0CT-2000
01-0CT-2000
                                                                                                                                                                                                      DOMAIN.
                                                                                                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
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SEQUENCE
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Matches
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01-MAY-2000 (TrENBIRE). 13, Created)
01-MAY-2000 (TrENBIRE). 13, Last sequence update)
01-UON-2001 (TrENBIRE). 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TOSIMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBErel. 13, Created)
01-MAY-2000 (TREMBEREL. 13, Last sequence update)
01-MAY-2001 (TrEMBEREL. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                      Gaps
                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                  21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human),
Sukaryota, Metazong Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoan Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                      4 ;
                                                                                                                                                                        GIPDRESGSGSGTDETLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKR 132
                                                                                                                                                                                             GIPDRESGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Vanyder Merwe P.L., Kalis N.N., Berney S.M., Young D.C.,
              Length 108;
Query Match 31.0%; Score 387; DB 4; Length 10
Best Local Similarity 65.2%; Pred. No. 1.6e-28;
Matches 73; Consergative 17; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.9%; Score 385.5; DB 4; Length 68.8%; Pred. No. 2.2e-28; tive 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243325F72C7DAC83 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98277139; hubmed-9614934;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF035028; AAD56264.1;
HSSP, P01789; IMCPS
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00359<u>6</u>; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.88
Matches 77; Conservative
                                           Conservative
                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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NON_TER 109 #109
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Query Match
                                                                                                                                                                                                                                                                 fetus.";
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                                                                                        Q9UL83
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                                                                  RESULT 10
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Q9UL81
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                                                            Clin. Immunol. Immunopathol. 87:184-192(1998).
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clin. Immunol, Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                          DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                        Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                           4,
                                                                                                                                                                                                                                                                                                   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                 30.7%; Score 384; DB 4; Length 108; 64.3%; Pred. No. 3e-28; 1ive 16; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 108;
                                                                                                                                                                                 11633 MW; B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AA; 11787 MW; DB5845F19724FB4E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.5%; Score 381; DB 4;
65.2%; Pred. No. 5.7e-28;
tive 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
                                                                                             EMBL; AF035044; AAD56280.1; -. HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PPR0047; 1g; 1.
SMART; SM00406; IGV; 1.
                                                                                                               InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF035035; AAD56271.1;
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Best Local Similarity 65.2%;
Matches 73; Conservative
                                                                                                                                                                                                                            Local Similarity 64.3 es 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                    Pfam; PF00047; 19; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                  DOMAIN.
                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
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Best Local S
Matches 72
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SEQUENCE
                                                    fetus.";
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Q9UL79
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO.IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOSLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoan Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutherian Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4,
81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKR 132
                     81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98277139; Rubmed-9614934;
Wu X., Liu B., Van-der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98277139; Rubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 373; DB 4; Length 108;
; Pred. No. 3.2e-27;
13; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AA; - 11834 MW; 9F9C5A92EBA96EEA CRC64;
                                                                                                                                           108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 AA.
                                                                                                                                                                               (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last seq
(TrEMBLrel. 17, Last ann
                                                                                                                                           PRT;
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Similarity 66.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; PO1607; IREI,
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF035031; AAD56267.1;
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                                                                                                                                           PRELIMINARY;
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SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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Gaps

21; Indels

21 DIVLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLES 80

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114 AA.

PRT;

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PRELIMINARY;
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NCBI_TaxID=6182;
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SEQUENCE
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Q9U410;
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Q9U410
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                         Query Match 29.3%; Score 365.5; DB 4; Length 107; Best Local Similarity 62.5%; Pred. No. 1.5e-26; Matches 70; Conservative 19; Mismatches 18; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 29.2%; Score 364.5; DB 4; Length 109; Best Local Similarity 65.5%; Pred. No. 2e-26; Matches 74; Conservative 13; Mismatches 21; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 GIPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRLEIKR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
              EMBL, AF035033; AAD56269.1; -.
HSSP; P80362; 1WTL.
INTECPPO: IPR003596; Ig_WHC.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
NON_TER 107 107
SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;
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109 AA; 11761 MW; FBIE43E7C7AFACCC CRC64;
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MEDLINE-98277139; PubMed-9614934;
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HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SMO0406; IGV; 1.
NON_TER
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NON_TER
SEQUENCE
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0991185
AC 0991185
DT 01-MAX DT 01-MAX DT 01-MAX DT 01-JUN DE MYOSIN OS CO MARIMAL OX MARIMAL DE MYOSIN RA WU X.,
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13

RESULT Q9UL80

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Clin. Immunol. Immunopathol. 87:184-192(1998).
-!- SIMILARITY: ToginmunoGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schistosoma japonicum.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
01.MAY-2000 (TIEMBLIE). 13, Created)
01.MAY-2000 (TIEMBLIE). 13, Last sequence update)
01.JUN-2001 (TIEMBLIE). 17, Last annotation update)
01.JUN-2001 (TIEMBLIE). 17, Last annotation update)
MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TREMBLrel. 17, Last annotation update)
MONOCLONAL ANTI-IDTOTPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
VARIABLE REGION (FRAGMENT).
Schistcosma japonicum (Blood fluke): Rhabditophora; Necdermata;
Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DIVLTQSPGTLSLSPGERATLSCKASQSVDY-DGDSYMNWYQQKPGQPPKLLIYAASNLE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SONG X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
Amplification, cloning and sequence analysis of the light chain
variable region gene of monoclonal anti-idiotypic antibody NP30 of
                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                 Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5,
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
WEDLINE-98277139; Rubmed-9614934;
WHU X., Liu B., Vander Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 AA; 12775 MW; 070E31E210D1CB01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

28.1%; Score 351; DB 4;
Best Local Similarity 58.8%; Pred. No. 3.7e-25;
Matches 67; Conservative 20; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN.

EMBL, AF207620; AAF19434.1; -
HSSP, P01679; 2FBJ.

InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffam; PF00047; 1g; 1.

SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035034; AAD56270.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; 1g; 1.
SMART; SM00406; 1Gy; 1.
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Job time: 288 sec

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1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                           23 VLTQSPGTLSLSPGERATLSCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGI 82
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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SEQUENCE FROM N.A.
Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
Chon Struction and sequencing of the single-chain antibody gene of human TNF-alpha specific monoclonal antibody.";
Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).

Mus musculus (Mouse).

Muscayota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae;                                                                                                                                                                                                                                                                          5;
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                                                                                                                                                                                     Length 106;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.7%; Score 334; DB 11; Length 107; 58.9%; Pred. No. 1.3e-23; ive 17; Mismatches 25; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 IPDRFSGSGSGTDFTLTIHPVEEEDAATYYCQQSNEDPRTFGQGTRL 128
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11478 MW; F20F544426BAE63E CRC64;
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                                                                                                                                                                   Query Match 27.6%; Score 344.5; DB 5; Best Local Similarity 61.5%; Pred. No. 1.4e-24; Matches 67; Conservative 13; Mismatches 24;
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InterPro; IPR003599; Ig.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
SMART; SM00409; IG; I.
SMART; SM00409; IG; I.
NON_TER
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Best Local Similarity 58.9%
Matches 63; Conservative
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106 J
NON_TER
SEQUENCE
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

SUMMAKLES		Description	AW83036 Anti-Fas humanised	AAB14776 Humanised anti-Fas	4	AW83037 Anti-Fas humanised		AAW90929 Humanised HFE7A de					
		3 ID		21 A	21 A	19 A	21 A	21 A	21 A	21 A	21 A	21 A	
	Query	ength D	470	470	470	470	470	470	470	470	470	470	(1)
de	Query	Match I	100.0	100.0	100.0	9.66	9.66	9.66	99.4	99.4	99.3	98.8	,
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AAB72228 AAB08026 AAB08025 AAX50166 AAX50166 AAX4446 AAX444319 AAX1023 AAX1023 AAX1023 AAX1023 AAX1023 AAX1023 AAX1023 AAX1020 AAX10
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2283.5 2279 2279 22779 22779 22775 2
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ALIGNMENTS

RESULT

аамв3036 ii AAW83036 standard; Protein; 470 АА. xx	AAW83036;		15-MAR-1999 (first entry)		Anti-Fas humanised antibody HFE7A heavy chain.	HPE7A: monoclonal antibody: mouse: Fas: humanised antibody:						_		atopy; arteriosclerosis; myocarditis; cardiomyopathy;				Homo sapiens.	Synthetic.			Peptide	/label= Sig_peptide	Protein 20470	/label- Mat_protein	Region		Region	/label= Constant
AA U X	¥ S	XX	DŢ	×	DE	X	KW	KW	KW	ΚW	ΚW	ΚW	Κ¥	ΚW	ΚW	ΚW	×	SO	SO	XX	FH	FT	FT	FT	F	FT	FT	FT	FI

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chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli pg451/A62 SANK 73397 harbors plasmid pg451/A62 carrying a fusion fragment of the humanised VD type HFE7A heavy chain and DNA as FERM bre6074 (claimed). The invention provides methods for producing humanised antibodies by culturing host cells. Humanised versions of HFE7A (see AAWR3031-37), like native HFF7A, are capable inducing apoptosis in abnormal cells expressing Fas, and of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells. The humanised antibodies are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia. Addison's disease, scleroderma, Goodpasture syndrome, crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, anayocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibodies and proteins bind conserved epitope of Fas antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of the VD type humanised heavy
                                                                                                                                                                                                                                                                                                                                                                                           Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 212-213; 292pp; English.
                                               69..84
/label- CDR_H2
/note= "claim 9"
118..129
/label- CDR_H3
                                    /note= "claim 9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myocarditis, hepatitis and AIDS
50..54
/label- CDR_H1
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97JP-0082953.
97JP-0169088.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV70079.
                                                                                                                                                                                                                                                 30-MAR-1998;
                                                                                                                                                                                                                                                                                                 01-APR-1997;
25-JUN-1997;
                                                                                                                                                                                                                                                                                    08-OCT-1997;
                                                                                                                                                                          AU9859701-A
                                                                                                                                                                                                              08-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                         Masahiko O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                         Akio S,
                                                     Region
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The invention relates to compositions for the prevention or treatment or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs (complementarity determining regions) to antibody HFE7A. Via its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases, allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rreventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody
240
                                                                                                                                241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                 301 YVDGVEVHNAKTKRREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                  KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                                                               421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB14776 standard; Protein; 470 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Mus musculus.
Chimeric - Homo saplens.
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N-PSDB; AAA72159.
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AAB14776
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glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. Sequences AAB14775-B14776 and AAB14779 represent the heavy chains (or fragments thereof) of various humanised HFE7A-derived anti-Fas antibodies.
                                                                                                                                                                                                                                                                                                                   KAKGOPREPOVTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV 420
                                                                                                                                                                                                                                                       YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                             WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                                                                                                                                                                                       241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                        YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kakgqprepqvyt1ppsreemtknqvs1tc1vkgfypsdiavewesngqpennykttppv 420
                                                                                                                                                                                                                                         GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                     Gaps
                                                                                                                                                                              1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                               ;
0
                                                                                                                       Length 470;
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                                                                                                                    Score 2515; DB 21;
Pred. No. 3.9e-143;
; Mismatches 0;
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100.0%;
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                                                                                                                                                  Matches 470; Conservative
                                                                                                                                    Similarity
                                                                         470 AA;
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Best Local (
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Mismatches

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Best_Local Similarity 100. Matches 470; Conservative

Query Match

Sequence

100.0%; Score 2515; DB 21; Length 470; 100.0%; Pred. No. 3.9e-143;

240

241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

241

ggrlewmgeidpsdsytnyngkfkgkatltvdtsastaymelss1rsedtavyycarnrd 120 121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180

WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP

181 181

GORLEWMGEIDPSDSYTNYNOKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120

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1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

ligand system, by:binding to Fas on the cell surface, and prevents

apoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,
anti-anemic, antidiabetic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosuppressive, thyromimetic,
antiarteriosclerofic, cardiant and hepatropic activity. (I) induce
antiarteriosclerofic, cardiant and hepatropic activity. (I) induce
antiarteriosclerofic, cardiant and hepatropic activity. (I) induce
inhibition of ligand binding (I) are used to treat and/or prevent
cardiant and binding (I) are used to treat soft prevent
cluseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, slorgermer, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
anitiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allery, arteriosclerosis, myocarditis,
cardiamyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis models. (I) act on the active site of Fas, i.e. they minic
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
a humanised anti-Fas antibody HEFA designed heavy chain which is used in
                                                                                                                                                                                                                                                                                              l anti-Fas antibody, useful for treating or preventing e.g. or autolmmune disease, induces apoptosis selectively in
                                                                                                                                                                       Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                              Example reference 15; Page 134-136; 263pp; English.
                                                                                                                                                                       Nakahara K, Tamaki I,
                                                                                                                                                                                                                                                                                            useful for
                                                                                                                                                                                                                                                                                                                                               cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                                                                                                                                              humanized anti-Fas antibody,
                                         98JP-0276881.
98JP-0276882.
99EP-0307711.
                                                                                                                                                                       Haruyama H,
                                                                                                                         (SANY ) SANKYO CO'LTD
                                                                                                                                                                                                                      WPI; 2000-258930/23
                                                                                                                                                                                                                                                N-PSDB; AAA11597.
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29-SEP-1999;
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                                                 30-SEP-1998;
30-SEP-1998;
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yvdgvevhnaktkpreegynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis 360
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YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                  KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                                          HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic luque erythematosus; graft versus host disease; Sjogrem syndrome; pernicious anaemia; Addison's disease; scleroderma: Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; insulin-dependent diabetes; allergy; attopia arterischeosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy.
                                                                            LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hiroko Y, Jun O, Kimihisa I;
S, Shin Y, Tohru T;
                                                                                                                                                                                Anti-Fas humanised antibody HFE7A heavy chain.
                                                                                                                                                                                                                                                                                                                                                  'label Sig_peptide
                                                                                                                                                                                                                                                                                                                                                         20..470
/label- Mat_protein
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                                                                                                                              AAW83037 standard; Protein; 470 AA
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/label= Variable
                                                                                                                                                                                                                                                                                                                                                                                                    'label - Constant
                                                                                                                                                                                                                                                                                                                                                                                                                              "claim 9"
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97JP-0169088
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O, Nobufusa
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                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                15-MAR-1999
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25-JUN-1997;
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Masahiko O,
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                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                AAW83037;
                                                                                                                                                                                                                                                                                                                                          Peptide
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This is the amino acid sequence of the HV type humanised heavy
chain of murine anti-human Fas monoclonal antibody HFB7A. It
includes humanising R446 and A767 amino acid substitutions that are
are conserved in the human 1969 heavy chain. Host Escherichia coli
pgHPDHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion
fragment of the humanised HV type HFB7A heavy chain and DNA
chocding humanised HV type HFB7A heavy chain and DNA
cas FERM BP-6273 (ctalaned). The invention provides methods for
producing humanised antibodies by culturing host cells. Humanised
versions of HFB7A*(see AAM83031-37). like native HFB7A, are capable
of inducing apoptosis in abnormal cells. The humanised
antibodies are used to evaluate, in animal models, treatments of
inhibiting Fas-induced apoptosis in normal cells. The humanised
antibodies are used to evaluate, in animal models, treatments of
treat such diseases, including autoimmune disease (e.g. systemic
clupus erythematosius, Hashimoto's disease, graft versus host disease,
lupus erythematosius, Hashimoto's disease, graft versus host disease,
clopen syndrome, pernicious anemia, sterility, myasthenia gravis,
autoimmune hemolytic anaemia, sterility, myasthenia gravis,
multiple scl rosig; Basedow's disease, thrombopenia purpura and
multiple cal rosig; Basedow's disease, thrombopenia purpura and
multiple cal rosig; And and transplant rejection (all clamed).
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                                                                                  antibodies and proteins bind conserved epitope of Fas antigen - it o evaluate drugs in animal models and to treat Fas-associated eases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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Pred. No. 1.8e-142;
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                                                                                                                                                                                                                                      Claim 22; Page 225$227; 292pp; English.
                                                                                                                                                                          myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.68;
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N-PSDB; AAV70080.
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LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSPGK 470 25 JULY 21. 15

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                                                                                                                                                                                                                                                                                                                                                             murine; humanised antibody; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; attopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis; hepatitis; AIDS; graft rejection; heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preventive or treating agent for the diseases caused by an abnormality in the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas antibody -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                                                                                                                                                                                                                                     Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
                                                                                                                                                                                                                                                                       Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 21; Page 108-109; 139pp; Japanese.
                                                                 AAB14779 standard; Protein; 470 AA.
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Chimeric - Homo sapiens.
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anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas; nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; crohn's disease; scleroderma; sterility; odogasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; giomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecule (I) that induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New humanized anti-fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in
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240
                                                                              360
                                                                                                                                                                                                         antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
                WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                               241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
                                                                                                                             YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS
                                                                                                                                                                                          KAKGOPREPOVETLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel humanized anti-Fas antibody-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi T;
                                                                                                                                                                                                                                                                          LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakahara K, Tamaki I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanised HFE7A designed heavy chain protein #2.
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N-PSDB; AAA11622.
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manusouractive, using consistent infuniosuppressive, informatic, antitrheumatic, nephrotropic, antiinfertility, neuroprotective, antiarheumatic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, Sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody HEPA designed heavy chain which is used in the method described in the Invention.
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Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;

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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that invention describes a poptosis in cells with an abnormal Fas/Fas molecule (I) that invention for an object of the invention and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, antidate of the invention have anti-inflammatory, immunodulatory, dermatological, antidated respective, thyromimetic, antidated activity, neuroprotective, immunodulatory, dermatological, antidifertility, neuroprotective, antistreniosclarothic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent capptosis by binding to cell surface Fas or inhibit it by competitive inhibit materials. (I) are used to treat and/or prevent competitive systemic systems sasociated with the Fas/Fas ligand system, especially systemic upus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic canemia, Addison's disease, theomotopenia purpura, insulin multiple sclerosis; Basedow's disease, thrombopenia purpura, insulin capender mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral (B, C or D) or alcoholic, and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they minic the native ligand, do not induce liver disease, and have reduced risk of the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-marine antibody reavy chain construct designated Heu I was a humanised anti-Fas antibody capen.
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                    anti-Fas;
                dermatological; immunosuppressive; thyromimetic; antirhemmatic; anti-re nephrotropic; antiinfertility; neuroprotective; antiantareriosoclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease, repeptosis; systemic lupus erythematosus; Sjorgen's syndrome; anemia; Addison's disease; soleroderma; sterility; Goodpasture syndrome; anemia; Addison's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopen'a purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; allomerulonephritis; hepatitis; transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively i
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Pred. No. 2.7e-142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakahara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 169-170; 263pp; English.
anti-arthritic;
                                                                                                                                                                                                                                                                                                                                                                            99EP-0307711.
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N-PSDB; AAA11644.#8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
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               420
                                                                                                                       KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                            YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
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                                           121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
                                                                                  WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
                                                                                                                                                                       GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD
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                                                                                                                                                                                                                                      Humanised anti-Fas designed heavy chain Heu 2 protein.
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                                                                                                                                                                                                                                                                                                           AA.
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98JP-0276882,
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30-SEP-1998;
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This invention describes a novel numanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-antidabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirarteriosclerotic, cardiant and hepatropic activity. (I) induce antirhematic, nephrotropic, antiinfertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand bhinding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic clubus erythematosus, Hashimoto disease, rhemmatoid arthritis, graft oversus host disease, solorgen's syndrome, pernicious or hypoplastic anemia, Addison's adisease, solorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, and transplant rejection. (I) selectively induce the nather and transplant rejection. (I) selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce lisease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 2 which is described in the method of the invention.
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                                                                  invention describes a novel humanized anti-Fas antibody-like
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Best Local Similarity 99.1%; Pred. No. 3.5e-142;
Matches 466; Conservative 2; Mismatches 2;
   English.
263pp;
Page 174-176;
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C$
   Claim
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AAW90935 standard; Protein; 470 AA. (first entry) WPI; 2000-258930/23. 29-SEP-1999; 08-AUG-2000 30-SEP-1998; EP990663-A2 05-APR-2000 30-SEP-1998 Serizawa N, Synthetic A COURT COUR

Fas; antibody; human; anti-inflammatory; anti-anemic; antidabetic; anti-allergic; anti-arthitic; antiviral; immunomodulatory; cardiant; dermatological; immunosuppressive; thyromimetic; antirheumatic; antin-Fas; nephrotropic; antiinfertility; neuroprotective; antiarteriosolerotic; hashlmoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; multiple solerosis; Basedow's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosolerosis; myocarditis; cardlomyopathy; glomerulonephritis; hepatitis; transplant rejection. Humanised anti-Fas designed heavy chain Heu 3 protein 99EP-0307711. 98JP-0276882. 98JP-0276881 (SANY) SANKYO CO LTD.

Haruyama H, Nakahara K, Tamaki I, Takahashi T;

N-PSDB; AAA11646

New humanized anti-Fas antibody, useful for treating or preventing e.g. inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems

Claim 2; Page 180-182; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cells surface, and prevents
c ligand system, by inhibiting binding between
Eas and its ligand. The products of the invention have anti-inflammatory,
anti-anemic, antidiabetic, antiallergic, anti-arthritic, antitiral,
anti-anemic, antidiabetic, antiallergic, anti-arthritic, antitiral,
anti-arterioscalerotic, cardiant and hepatropic activity. (I) induce
antiarterioscalerotic, cardiant and hepatropic activity. (I) induce
antiarterioscalerotic, cardiant and hepatropic activity. (I) induce
antiarterioscalerotic, cardiant and hepatropic activity. (I) induce
c inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
clubus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, soleroderma, Goodpasture syndrome, Cohn's
canemia, Addisease, scleroderma, Goodpasture syndrome, Crohn's
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
continuity apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanised anti-Fas antibody heavy chain construct designated Heu 3 which is described in the method of the invention.

470 AA; Sequence

CO. LID.

(SANY) SANKYO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 KAKGQPREPQVYILPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
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                                                                                                                                                         Length 470;
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                                                                                                                                                                                   Indels
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                                                                                                                                                 8; DB 21;
4e-142;
                                                                                                                                                      Score 2498; DE Pred. No. 4e-142; Mismatches
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                                                                                                                                                       99.3%;
99.1%;
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98JP-0276882.
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                                                                                                                                                          Query Match
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361 kakgqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennykttppv 420

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AAW48650 standard; Protein; 652

11

AAW48650

Antibody-cytokine fusion protein; tricistronic vector; chimeric; TNF alpha; IL-2; TRES; internal ribosome entry site.

Heavy chain of hmAb425 fused to TNF alpha.

(first entry)

04-AUG-1998

AAW48650;

/note= "Heavy chain of human mAb 425"

495..652 /note= "TNF alpha"

WO9811241-A1

19-MAR-1998

02-SEP-1997; 30-SEP-1996; 16-SEP-1996;

Location/Qualifiers

Homo sapiens

Synthetic

..494

Region Region

Key

9

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This invention describes a novel humanized anti-Fas antibody-like

molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
completes in cells with a normal system, by inhibiting binding between
camportosis in cells with a normal system, by inhibiting binding between
campination cells with a normal system, by inhibiting binding between
canti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosupressive, thyromimetic,
antirheumatic, nephrotropic, antilnfertility, neuroprotective,
cantiarterioscleroric, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
capoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
capoptosis by binding to cell surface Fas or inhibit it by competitive
capottosis assasses, scleroderma, coodpasture syndrome. Crohn's
culpus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
culpus erythematosus, Hashimoto disease, theumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, crohn's
classase, addison's disease, thrombopenia purpura, insulin
disease, allergy, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, theritis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they minic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
the humanised anti-Fas antibody HEFA heavy chain construct HHH type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                New humanized anti-Fas antibody, useful for treating or preventing inflammatory or autoimmune disease, induces apoptosis selectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
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       Takahashi T;
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Pred. No. 2.4e-141;
3; Mismatches 4;
       Tamaki I,
                                                                                                                                                                                                                                                              cells with abnormal Fas-Fas ligand systems
   Nakahara K,
                                                                                                                                                                                                                                                                                                                             Claim 2; Page 188-189; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.8%;
98.5%;
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   Нагиуаша
                                                                      2000-258930/23
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                                                                                                         N-PSDB; AAA11655
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The present sequence represents a fusion protein comprising of TNF alpha fused to the C-terminus of the heavy chain of the human monoclonal antibody 425 (hmab425). The hmab425 has specificity for the human EGF receptor. The invention claims for a new pMCLDHAP tricistronic vector (AAV18096) for the expression of an antibody-cytokine fusion protein, hmab425-TNF alpha. The TNF alpha sequence can be substituted by the IL-2 sequence. The vector also contains a strong promoter/enhancer unit, a selection marker gene and ileast two poliovirus derived internal ribosomal entry site (IRES) sequences. The vector can be expressed in mammanian host cells for the production of heteromeric fusion proteins. This expression system is claimed to produce the heteromeric proteins in high yields.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligo:cistronic expression vector - useful for production of, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKRPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 652;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.0%; Score 2288; DB 19;
ilarity 87.5%; Pred. No. 2.1e-129;
Conservative 17; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 15; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              , Burge C, Dunker R,
Von Hoegen I, Welge T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-207400/18.
N-PSDB; AAV18096.
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Best Local Similarity
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YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360

KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW

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KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420

Mielke C;

Hauser H,

96EP-0115635. 96EP-0114820. 97WO-EP04765

(MERE) MERCK PATENT GMBH.

Bruenmer W,

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Sequence
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                                                                               215
                                                                                     LGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLM 275
                                                                                                                      ISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD 335
                                                                                                                                                     Combination for treating cancer (e.g. breast, gastric or prostate cancers), or in the manufacture of a medicament for anti-cancer therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody with a chemotherapeutic agent.
                                                                                                                                                                                                                                                                                                                                                               synthesis;
9
1 mdwtwrvfcllavapgahsqvqlvqsgaevkkpgasvkvsckasgytftshwmhwvrqap
                                               -----ASTKGPSVFPLAPSS
                                                                              KSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS
                                                                                                                                                                             WINGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGF
                                                                                                                                                                                                            YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
                                                                                                                                                                                                                                                                                                                                               Humanised 323/A3 (IgG1) antibody heavy chain amino acid sequence
                                                                                                                                                                                                                                                                                                                                                             Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synth chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
                                              YS-NNWYFDVWGEGTLVTVSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thurmond LM
                                                                                                                                                                                                                                                                                                AAB72228 standard; Protein; 465 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 16; 103pp; English
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                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                           HNHYTOKSLSLSPGK 470
                                                                                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stimmel JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-182729/18.
N-PSDB; AAF63374.
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200107082-A1.
                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                               heavy chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knick VC,
                                                                                                                                                                                                                                                                                                                 AAB72228;
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This invention relates to a combination of an anti-Ep-CAM (cyclic adenosine monophosphate) antibody with a chemotherapeutic agent, that is adenosine monophosphate) antibody with a chemotherapeutic agent, that is phase or the second growth phase (M) of cell enlargement (G2)/DNA replication. The antibody exhibits cytostatic activity and is useful in the manufacture of a medicament for use in anti-cancer therapy, characterised in that a chemotherapeutic agent, which is capable of arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-administered to a patient with an anti-Ep-CAM antibody. The combination is useful for treating cancer, prostate cancer or non-small-cell ung cancer. The present sequence represents the heavy chain of anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be used in the combination of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; 1gG; complement system; Fcgamma receptor; cytotoxic effector cell; host immune cell; programmed cell death; allergic disorder; cancer; autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease; allergic bronchopulmonary aspergillosis; allergic rhinitis; cancer; Graves's disease; food allergy; allergic contact dermatitis; cancer; B-cell lymphoma; wheumatoid arthritis; ulcerative colitis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAKGOPREPQVYŢLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.8%; Score 2283.5; DB 22; Lengt
91.7%; Pred. No. 2.8e-129;
ive 14; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dimeric anti-CD20 heavy chain polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 431; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180

121 121 181

> 셤 ŏ

241 kscdkthtcppcpapellggpsvflfppkpkdtlmisrtpevtcvvdvshedpevkfnw 300

241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW

> g δy 셤 ŏ g

WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP

YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS

301

360

240 240 300

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polypeptide. The dimeric immunoglobulin is used in the method of the invention. The specification describes a method for producing an immunoglobulin (1g) G/IGG dimer. The method comprises genetically engineering a monoclonal antibody to introduce a cysteine molecule which inhibits formation of intramolecular disulphide bridges between sister heavy chains on the same antibody molecule. The dimer is a homodimer or heterodimer that is capable of activating components of the complement system, and has the ability to activate and kill cells via the complement cascade. The dimer is also capable of binding to Fegamma receptors on cytotoxic effector cells and on host immune cells, and is capable of initiating programmed cell death. The IgG/IgG dimers may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to treat allergic disorders, cancers and autoimmune diseases such as allergic asthma, allergic bronchopulmonary aspergillosis, allergic rhinitis, atopic dermatitis, crohn's disease, Graves's disease, food allergies, allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They may also be used to treat a range of other diseases and disorders such as rheumatoid arthritis, lorentive colitis, psoriasis, pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis and aplastic anaemia. They are also useful for inducing hyper-cross-linking of membrane antigens and for the preferential killing of selected cell populations.
                                                                                                                                                                                               /note= "murine anti-human CD20 heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genetically engineering immunoglobulin (Ig) G/IgG dimers for the treatment of cancers, allergic disorders and autoimmune conditions
                                                                                                                                                                                                                                    141..470
/note= "human gamma 1 heavy chain constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents a dimeric anti-CD20 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hariharan K, Labarre MJ, Huynh TB;
pigeon breeder's disease; hepatitis; leprosy; Lyme disease; diabetes mellitus; candidiasis; aplastic anaemia.
                                                                                                                                                    /note= "signal peptide"
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 2A-C; 65pp; English.
                                                                                                                                                                                                                   region"
                                                                                                                                                                                                                                                                                                                                                                                                               99US-0238741.
                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2000; 2000WO-US01893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Braslawsky GR, Hanna N,
                                                                                                                                                                           .140
                                                         Mus sp.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IDEC-) IDEC PHARM CORP
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                                                           Mus
                                                                                                                                                                                                                                                                                               WO200044788-A1.
                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-1999;
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                                                         Chimeric -
Chimeric -
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                                                                                                                                  Peptide
                                                                                                                                                                                                                                      Protein
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This invention relates to a combination of an anti-Ep-CAM (cyclic adenosine monophosphate) antibody with a chemotherapeutic agent, that is capable of arresting Ep-CAM antigen expressing cells in the synthesis (S) phase or the second growth phase (Gell enlargement (G2)/DNA replication. The antibody exhibits cytostatic activity and is useful in the manufacture of a medicament for use in anti-cancer therapy, characterised in that a chemotherapeutic agent, which is capable of arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-administered to a patient with an anti-Ep-CAM antibody. The combination is useful for treating cancer, particularly colorectal
KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
             Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis; chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Combination for treating cancer (e.g. breast, gastric or prostate cancers), or in the manufacture of a medicament for anti-cancer therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody with a chemotherapeutic agent -
                                                                                                                                                                                                                                                                               Humanised 323/A3 (IgG1) antibody heavy chain amino acid sequence.
                                                                                421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thurmond LM;
                                                                                                                                                                               AAB72232 standard; Protein; 464 AA
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                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stimmel JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-182729/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200107082-A1.
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                  heavy chain.
                                                                                                                                                                                                                                                10-MAY-2001
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Gaps

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Indels

26; DB 21;

Length 470;

Score 2279; DB 21; Pred. No. 5.2e-129; 17; Mismatches

90.6%;

Matches 427; Conservative

Similarity

Query Match Local

61 GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120

61

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1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60

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Sequence
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 cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell ung cancer. The present sequence represents the heavy chain of anti-Ep-CAM antibody known as humanised 323/A3 (IgGl) which can be used in the combination of the invention.
                                                                                                                                                                                                                                                                                                   GORLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                           121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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9991ewmgwintytgeptygedfkgrfafsldtsastaymelsslrsedtavyfcar--- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                 Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy; glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody; human; immunoglobulin G; IgG; heavy chain region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142..466 "Derived from human IgG heavy chain constant region"
                                                                                                                                                                                                                          1 MGWSCIILFIVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                            5;
                                                                                                                                                       22; Length 464;
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/note= "Derived from mouse heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469
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Pred. No. 5.5e-129;
Transport of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric 2403 IgG antibody heavy chain (5F2.4H4.1E3).
                                                                                                                                        90.6%; Scor.
91.7%; Pred. No. 5...
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..19
/label= Signal_peptide
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                                                                                                                                                 Query Match
Best Local Similarity 91.73
Matches 430; Conservative
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- Homo sapiens.
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                                                                                             464 AA;
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                                                                                             Seguence
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Chimeric
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The present chimeric sequence is full length 2403 immunoglobulin G (1gG) antibody heavy chain (5F2.4H4.1E3) derived from murine heavy chain variable region (VL) and human 1gG heavy chain constant region.

This antibody binds to prostate stem cell antigen (PSCA) which is a single subunit glycoprotein that is expressed on the cell surface as a glycosylphosphatidylinositol (GPI)-anchored protein. The present invention relates to anti-PSCA antibody composition and methods of killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and killing the growth of PSCA-expressing cancer cells such as prostate cancer. bladder cancer or lung cancer cells. Humanised antibody conjugated to a toxin or a radioactive isotope is used for killing the cancer cells in vivo and for inhibiting or killing these cells. The antibodies are also useful for treating the above mentioned cancers and for immunoprecipitation of PSCA-expressing cancer. for purification of pSCA from cells, and for detection and quantitation of PSCA in vitro. PSCA NoA is also useful for treating cancers by gene therapy techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    internalizes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel anti-prostate stem cell antigen (PSCA) antibody that ion binding to PSCA on mammalian cell and inhibits growth of PSCA-expressing cancer cells in vivo, useful for killing PSCA-expressing cancer cells in vivo, useful
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Pred. No. 8.9e-129;
7; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                    Lasky
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                                                                                                                         27-OCT-2000; 2000WO-US29603
                                                                                                                                                                                       29-OCT-1999; 99US-0162558
16-FEB-2000; 2000US-0182872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 427; Conservative
                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                    Devaux B, Keller G,
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-389954/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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WO200140309-A2
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Sequence 7, Appli Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 12, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 12, Appli

App1 App1

Sequence

Sequence 4, Appli Sequence 12, Appl Sequence 8, Appli Sequence 10, Appl

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Sequence 13, Application US/08458516
Fatent No. 5777085
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: TSO, Man Sung
APPLICANT: TSO, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: GPIIB/IIIA
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
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                                                                                                    US-08-397-411-7
US-08-487-550-4
PCT-US-6-10043-9
US-08-461-968A-5
US-08-461-968A-5
US-08-480-036-2
US-08-480-036-2
US-08-461-968A-2
US-08-461-968A-2
US-08-461-971-2
                                                      US-08-341-560B-17
US-08-487-550-12
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US-08-523-894-12
                                                                                                                                                                                                                                                                                                                                                                                                               US-08-523-894-8
US-08-523-894-10
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPRAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
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2047.5
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1937
1867.5
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        (without alignments)
251.344 Million cell updates/sec
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22, Appl
22, Appl
14, Appl
16, Appl
18,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-378-939-10

US-09-04-46-7-1

US-09-027-449-7-1

US-09-026-985-71

US-08-437-6428-22

US-08-437-6428-22

US-08-437-6428-22

US-08-437-6428-14

US-08-887-3528-14

US-08-466-15-165

US-09-109-207C-16

US-09-296-005-14

US-09-296-005-16

US-08-487-550-8

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US-07-934-373C-23
US-08-437-642B-23
US-08-157-101A-7
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Minimum DB seq Maximum DB seq

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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Best Local Similarity 92.5 Matches 417; Conservative

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2087.5 2083.5 2080.5 2080.5 2079.5

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Query Match

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                                                                            140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 199
                                                                                                                                           119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSCVHTFPAVLQS 178
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                                                                                                                                                                                                          GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                       239 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEGY
                  EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1...
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/378,939
FILING DATE:
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N.W.
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PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEFAN: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF,
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/08378939 Patent No. 5876961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: ROTHWELL, FIGG, ER
STREET: 555 THIRTEENTH ST. N.
CITY: WASHINGTON
STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
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LENGTH: 476 amino acids
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TOPOLOGY: linear
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                                                                  Length 476;
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                                                                  88.0%; Score 2214; DB 2;
87.8%; Pred. No. 3.8e-164;
ive 22; Mismatches 30;
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STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Gorley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TILLE OF INVENTION: HUMAN IMMUNE SY
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09049672A
Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                     Best_Local Similarity 87.8
Matches 418; Conservative
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MEDIUM TYPE: Diskette
protein
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PRIOR APPLICATION DATA:
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US-08-378-939-10
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South San Francisco
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US-09-026-985-71
                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGAL 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 REPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 ILFLVATATGVHSQVQLVQSGAEVKKPCASVKVSCKASGYTFTSYWMQWVKQAPGQRLEW 66
                                                                                                                                                                                                                                                                                                                                                                                                3;
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APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                          Length 467;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467
                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                     28;
                                                                                                                                                                                                                                                                                                                       87.3%; Score 2195.5; DE
89.0%; Pred. No. 1e-162;
11ve 20; Mismatches 2
                                         NAME: Cerrone, Michael C
RECISTRATION NUMBER: 39,132
REFERNCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 71, Application US/09027449 Patent No. 6025158 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                             INFORMATION FOR SEQ ID NO: 8:
                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 89.0°
Matches 413; Conservative
                                                                                                                                                                                                                                                ; LIBRARY: LUNGTUT11
; CLONE: 2747531
US-09-049-672A-8
APPLICATION NUMBER:
                                                                                                                                                                                                                                IMMEDIATE SOURCE:
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US-09-027-449-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   319 YNSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQRLEWMGEIDPSDSYTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.1%; Score 2189.5; DB 3
89.6%; Pred. No. 2.8e-162;
iive 28; Mismatches 18;
                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy dis COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/027,449 FILING DATE: 20-Feb-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                 P1085R3-2
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTONIEY/AGENT INFORMATION:
NAME: LOVE, RICHARD B.
REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 71: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     650/225-5530
650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 452 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 89.63
Matches 405; Conservative
                                     COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
USA
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US-07-934-373C-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELL
                                        APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Deng, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 87.1%; Score 2189.5; DB 4; Best Local Similarity 89.6%; Pred. No. 2.8e-162; Matches 405; Conservative 28; Mismatches 18;
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                              P1085R3-1
                                                                                                                                                                                                                                                                                                                  MBER: US/09/026,985
20-Feb-1998
Sequence 71, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               34,659
                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 71:
                                                                                                                                                Genentech, Inc.
                                                                                                                                                                           CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      650/952-9881
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                             1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                         USA
                                                                                                                                                                                                                     94080
                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-026-985-71
                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                             STREET:
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LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.7%; Score 2155.5; DB 2
89.2%; Pred. No. 1.2e-159;
Live 17; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P0709P2
US-07-934-373C-22; Sequence 22, Application US/07934373C; Patent No. 5821337; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       Genentech, Inc.
                                                                                                                                                                                                                                        CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 454 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 89.2%
Matches 405; Conservative
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                                                                                                                                                                              CORRESPONDENCE ADDRESS: ADDRESS:
                                                                                                                                                                                                                      STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                            USA
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181 LOSSGLYSLSSVVTVPSSSLGTQTYICHVHKPSNTKVDKKVEPKSCDKTHTCPPCPAPE 240
                                                                                                                                                                                                              257 LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
                                                                                                                                                                                                                                                                                                                                                                            NOKFKGKATLIVDISASTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGEGTLV 136
                                                                     TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV 196
                                                                                       LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPE
                                                                                                                                                                                                                                EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                                                                                                     377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:

INTLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                              437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSILIANTION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-70N-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
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CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION)
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 15-JUN-1992,
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 07/9
FILING DATE: 21-40G-1992
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 199308
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                  EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
                                                                   SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                              APPLICANT: Paul J. Carter
APPLICANT: Paul J. Carter
TITLE OF INVENTION: Immunoglobulin Variants
UNMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                      437 KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                       17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: PCT/US92/05126
15-JUN-1992
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV 1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               Sequence 22, Application US/08437642B Patent No. 6054297
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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US-08-437-642B-22
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TELEFAX:
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                               NQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRDYSNNW---YFDVWGEGTLV 136
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                                                                                                                                                                                                                             LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
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                                                                                                              20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQRLEWMGEIDPSDSYTNY 79
                                                                                                                             EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                         3,
                                                                DB 5; Length 454;
                                                                                         Indels
                                                                                         29;
                                                            85.7%; Score 2155.5; DB 389.2%; Pred. No. 1.2e-159, live 17; Mismatches 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPERSIBLE PC-DOS/MS-DOS
SOFTWARE: Winharin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
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REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                         Best Local Similarity ....
Matches 405; Conservative
 amino acid
; TYPE: amil
; TOPOLOGY:
PCT-US93-07832-22
                                                             Query Match
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Sequence 16, Application US/08887352B

Patent No. 5994511

GENERAL INFORMATION:
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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                                                                                                                                                                                     Length 451;
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                                                                                                                                                                                Score 2113; DB 2;
Pred. No. 2.4e-156;
5; Mismatches 31;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-Jul-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
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                   14:
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87.2%;
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CITY: South San Francisco
STATE: California
COUNTRY: USA
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
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                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Svoboda, Craiq G
                                                                                                                                                                                                                           Conservative
650/952-9881
                                                                                               ; TOPOLOGY: Linear
US-08-887-3528-14
                                                                                                                                                                                Query Match
Best Local Similarity
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TOPOLOGY:
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87.2%; Pred. No. 2.4e-156;
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Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC COMPATIBLE
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 39,044
REPERENCE/POCKET NUMBER: P112.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
FELERAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                           TOPOLOGY: 1:451 amino acids
TYPE: Amino Acid
BRA...
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US-08-466-151-65
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87.2%; Pred. No. 2.4e-156;
11ve 25; Mismatches 31;
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US-09-109-207C-14
Sequence 14, Application US/09109207C
Petent No. 6172213
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07/879495
                                                                                                                                                          APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
                                                                                                                                                                                                                                                                                                                     08/185899
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TELECOMMUNICATION INFORMATION
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/185
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879
FILING DATE: 07-MAY-1992
PRIOR APPLICATION NUMBER: 07/744
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/46
FILING DATE: 06-Jun-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39
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Sequence 14, Application US/09296005
Fatent No. 6290957
GENERAL INFORMATION:
FALE APPLICANT: Henry B.
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptil
FILE REFERENCE: P1123G1r
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT APPLICATION NUMBER: US/09/296,005
CURRENT FILING DATE: 1999-04-21
EARLIER FILING DATE: 1999-04-21
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                      79 YNOKFKGKATLIVDISASTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVIV 138
                                                                                                                                                                                                                                                                                                                             299
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                            ; NAME/KEY: Artificial
LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-16
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                                                                                                                                           84.0%; Score 2113; DB 4;
87.2%; Pred. No. 2.4e-156;
tive 25; Mismatches 31;
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Matches 394; Conservative
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Patent No. 6172213
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptide
FILE REFERENCE: P1123R1
CURRENT APPLICATION NUMBER: US/09/109, 207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/051,554
PRIOR PAPLICATION NUMBER: US 60/051,554
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 16
LENGTH: 451
TYPE: PRT
ORGANISM: Artificial
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptide FILE REFERENCE: P1123R1
CURRENT PPPLICATION NUMBER: US/09/109,207C
CURRENT PPLICATION NUMBER: US 60/051,554
PRIOR APPLICATION NUMBER: US 60/051,554
NUMBER FILING DATE: 1997-07-03
NUMBER FILING DATE: 1997-07-03
SEQ ID NOS: 44
SEQ ID NOS: 44
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87.2%; Pred. No. 2.4e-156;
ive 25; Mismatches 31; Indels
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Best Local Similarity 87.2%
Matches 394; Conservative
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                                                                                                                                                                                                                                                          NAME/KEY: Artificial LOCATION: 1-451
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Patent NO. 6290957
GENERAL INFORMATION:
APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
TITLE OF INVENTION: Improved Anti-1gE Antibodies and Method of Improving Polypeptides
FILE REFERENCE: P1123G1r
CURRENT APPLICATION NUMBER: US/09/296,005
EARLIER APPLICATION NUMBER: US 08/887,352
EARLIER APPLICATION UNMBER: US 08/887,352
EARLIER FILING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 26
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                                      YNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTV
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Matches 394; Conservative
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US-09-296-005-16
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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protein search, using sw model OM protein -

Search time 49.97 Seconds (without alignments) 716.471 Million cell updates/sec April 24, 2002, 15:11:37; Run on:

US-09-499-662-89 2515 1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470 Title: Perfect score: Sequence:

219241 segs, 76174552 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

219241 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ig gamma-1 chain C
Ig gamma-3 chain C
Ig gamma-2 chain C
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G1MSM G3MSM

Ig gamma-2a chain Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig mu chain precur	Ig heavy chain pre	Ig heavy chain (DO	Ig gamma chain - m	Ig gamma-1 heavy c	Ig heavy chain VHI	Ig Y heavy chain (
G2MSA S00847	G2MSAB	G2MSAM	PS0019	S06611	G2MSBM	147162	S38864	S14683	S04845	S69131	S38950	A49444	569340	B46529
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ALIGNMENTS

	RESULT 1
	Ig gamma-1 chain C region - human
	C.Species: Homo sapiens (man) C.Date: 31-Jan-1981 #secuence revision 18-Aug-1982 #text change 16-Jul-1999
	C; Accession: 234843; 234841. 2338845. B90563; A90564; B91668; A91723; A02146
	Kitilison, J.W.; Berson, B.J.; Hood, L.E. Nucleic Acids Res. 10, 4071-4079, 1982
	A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene. A;Reference number: A93 433; MUID:82274238
	A; Accession: A93433
	A;Molecule type: DNA A;Residues: 1-330 <ell></ell>
	A;Cross-references: EMBL:217370 A:Note: this commons has the Clm/17, allotunic marker 07-10s and the Glm/1, marke
	A; Note: Lys-330 is removed after translation
	K;HBITIS, LJ. c.whmitted to the DMDI Data Library October 1902
	Substance of the man back around; October 1992 A; Reference number: S33904
	A, Accession: S36861
	A MOLECULE type: DNA A. Docidinge: 2.230 (unab.
	A. Cross references: EMBL: 217370
	R; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
	Cell 29, 671-679, 1982
	Artitle: Structure of human immunoglobulin gamma genes: implications for evolution o
	A; Keterence number: 53388/; MULD:85001943 A:Acression: 533887
	A. Molecule type: DNA
	A; Residues: 88-113; 235-330 <tak></tak>
	A;Cross-references: EMBL:Z17370
	R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelm
	BIOCHEMISETY 9/ 3161-3110, 19/0 A.mista of a bunnar gammaC.immunocalobulin VII Amiso acid on
	A, Tarte: Lime Covernetts State Care a munical gainmen Timmunoy100041111. VII. Amilio acta Se A. Reference number: A90563; MUID:71064024
	A;Contents: myeloma protein Eu
	A A Accession: B90563
	A; Nolecule Cype: Pioceth A: Residnes: 1-96, 'R', 98-135 <cin></cin>
	A, Note: this sequence has the Gim(3) marker, 97-Arg
	R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
	A/TILE: The Covalent structure of a numba gammaG-lumnunoglobulin. VIII. Amino acid s is Reference number: 100664. WITH: 71064035
	A; Contents: Bu
	A; Accession: A90564
	A;Molecule type: protein A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',
	A; Note: this sequence has the G1m(non-1) markers, 239-G1u and 241-Met
	Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
-	A;IILLE: DIE FIIMAEFSTUKTUT EINES MONOKIONAIEN 19G1-IMMUNGIODULINS (MYELOMPTOCEIN F

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C;Accession: A23511
R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A;Hitle: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            u) with an IGHG4 conv
                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C;Genetics:
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                                                         Ig gamma-3 chain C region (allotype G3m(b)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec:1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
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C.Jacester 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C.Jacession: A60764
R.Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A.;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an lA;Reference number: A60764; MUID:90007613
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A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin c region; immunoglobulin homology C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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Pred. No. 5.5e-87
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82.8%;
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A;Cross-references: GDB:119339;
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Best Local Similarity
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A; Residues: 1-377 <HUC>
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                                                                            A; Residues: 1-34, 'O', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240,'L', 242-268, 'E', 27
A; Residues: 1-34, 'O', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240,'L', 242-268, 'E', 27
A; Note: this sequence has the Gim(1) and Gim(1) markers
R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A; Title: Die Primaerstruktur des Kristallsierbaren monoklonalen Immunglobulins IgG1 KOL
A; Reference number: A91723; MUID: 3329131
A; Molecule type: protein
A; Reference number: A9173; MUID: 332913
A; Molecule type: protein
A; Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
R; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide
A; Ritle: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide bonds
A; Title: The covalent structure. The primary structure of monoclonal IgG1 immunoglob
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Rieference number: A91667; MUID: 7700267
A; Contents: annotation: disulfide bridges.
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A:Contents: annotation; disulfide bonds
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A:Gross-references: GDB:120085; OMIM:147100
A:Map position: 14932.33-14932.33
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Pred. No. 7.9e-94;
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A;Contents: myeloma protein Nie
A;Accession: B91668
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99.18;
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Best Local Similarity
Matches 327; Conserv
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Across references: GDB:119338; OMIM:147110
A;Map position: 14q32.33-14q32.33
A;Map position: 14q32.33-14q32.33
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (c):Complex: An immunoglobulin heterotetramer sigh and IgM, the subunits associate into c;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85,Domain: immunoglobulin homology <IML>
F;239-305/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
                                                                                                                                                                                                         and 264-268
60-Ala and in the ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83.48-200.246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;106/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: $37483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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Blochem J. 127, 217-225, 1971
Blochem J. 127, 217-225, 1971
A; Title: Disulphide bridges of the heavy chain of human immunoglobulin A; Reference number: A90253; MUID:72033500
A; Contents: annotation; myeloma protein Sa, disulfide bonds
R; Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A; Title: Structural studies of immunoglobulin G.
A; Reference number: A93157; MUID:69064124
A; Contents: annotation; Sa, disulfide bonds
                                                                                                                                                                                                         A; Contents: annotation; Zie, revisions to residues 25, 59, 60, A; Note: the revised sequence differs from that shown in having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1610; DB 1;
Pred. No. 2.3e-85;
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     number: A93132; MUID:80114419
                                                                                                                                                         March 1980
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91.8%;
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                                                                             A; Molecule type: protein
A; Residues: 238-275 < HOF>
R; Hofmann, T:; Parr, D.M.
submitted to the Atlas, Man
A; Reference number: A94591
                                                     A; Accession: A93132
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A; Gene: GDB: IGHG2
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Best Local Si
Matches 303;
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A;Residues: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A;Residues: 1-24, E', 26-57, EV', 60-85;132-171, 'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
R;Note: this sequence has since been revised
R;Hofmann, T.: Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
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C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain A;Reference number: A93906; MUID:82197621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056 A;Nofe: Lys-326 is probably removed posttranslationally R;Wang, A.C.; Tung, E.; Fudenberg, H.H. R;Wang, A.C.; Tung, L. 125, 1048-1054, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The primary structure of a human 1gG2 heavy chain: genetic, evolutionary, A;Reference number: A92809; MUID:81007873
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19, (2,21-57,2,259,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can, J. Blochen: 57, 758-767, 1979
A;Fitle: The amino acid sequences of the three heavy chain constant region domains of R;Reference number: A90752; MUID:80001357
                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                          121 DIPPPCPRCPEPKSCDIPPPCPRCPEPKSCDIPPPCPRCPAPELLGGSVFLFPPKPKDI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 453
                                                                                                                                                                                                         141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                           Gaps
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                                                                                                                                                           47;
                                                                                                      Length 377;
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                                                                                                        DB 2;
                                                                                                                                                           11;
                                                                                                   Score 1637.5; DB
Pred. No. 7.2e-87;
7; Mismatches 11
C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMM>
                                                                                                      65.1%;
82.8%;
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Matches 312; Conservative
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A; Residues: 1-326 <ELL>
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                                                                                                        Query Match
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A; Molecule type: DNA
A; Residues: 138-161, 'L', 163-189, 'FP', 193-474 < YAM>
A; Cross-references: GB: 100461
A; Oto: the sequence was determined from the germline 9
R; Tucker, P. W.; Marcu, R.B.; Slightom, J.L.; Blattner, Science 206, 1299-1303, 1979
                                                                                                                                                     <IM2>
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                                                                                                                                                 F;134-203/Domain: immunoglobulin homology F;240-307/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                     Query Match 63.6%;
Best Local Similarity 91.8%;
Matches 303; Conservative
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Best Local Similarity
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                   A; Reference number: S37483
A; Reference number: S37483
A; Status: preliminary
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-469 < DUC>
A; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                               121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                     241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
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                                                                                                                                                                                                                    Length 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Homo sapiens (man)
C.Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change
C.Accession: A90933; A90249; A02150
R.Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4
A;Reference number: A90933; MUID:83157104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Received type: DNA
A; Residues: 1-327 < ELL>
A; Note: the sequence was determined from the germline gene
B; Pink. J. R. L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A; Title: Human immunoglobulin sublclasses. Partial amino ac
A; Reference number: A90249; MUID:70207560
                                                                                                                                                                                                           63.7%; Score 1602.5; DB 2; ilarity 64.2%; Pred. No. 9.3e-85; Conservative 60; Mismatches 104;
          Library, February
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A; Residues: 1-30;81-326 <PIN>
        submitted to the EMBL Data
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Best Local Similarity
Matches 303; Conserv
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A; Gene: GDB: IGHG4
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A introns: 99/1; 111/1; 221/1
A introns: 99/1; 111/1; 221/1
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C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1980 #Sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Date: 31-Mar-1980 #Sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: S25057; A02157; A26235; A26233; A35398
R;Fischer, R; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi
A;Reference number: S25057
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A;Molecule type: mRNA
B;Molecule type: mNO
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Pred. No. 9.2e-85;
9; Mismatches 15;
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1g gamma-za cnain (madz)-3) - menuse
C. Species: Mus musculus (house mouse)
C. Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C. Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C. Accession: $4025
R. Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C submitted to the EMBL Data Library, January 1993
A. Reference number: $40295
A. Accession: $40295
A. Accession: $40295
A. Reference number: $40295
A. Reference number: $40295
A. Reference number: $40295
A. Reference number: $40295
A. Residues: 1-446 < KLE>
C. Genetics:
A. Rep position: 12
A. Rep position: 12
A. Rep position: 12
A. Rep position: 12
C. Superfamily: immunoglobulin C region; immunoglobulin; pyroglutamic acid
F.: 1-11/Toomain: U-D-J region < CHR>
F: 118-446/Toomain: C region < CHR>
F: 118-144/Domain: C1 region < CHR>
F: 118-144/Domain: C2 region < CHR>
F: 118-144/Domain: C2 region < CHR>
F: 1215-230/Region: hinge
F: 231-340/Domain: C3 region < CHR>
F: 360-427/Domain: 1mmunoglobulin homology < IMM>
F: 360-427/Domain: immunoglobulin homology < IMM>
F: 125-296.144-199, 261-321.367-425/Disulfide bonds: interchain #status predicted
F: 1227, 229/Disulfide bonds: interchain #status predicted
F: 127, 229/Disulfide bonds: interchain #status predicted
F: 227, 229/Disulfide bonds: interchain #status predicted
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                                                                                                                   NOKFKGKATLIVDISASTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLVTVS 139
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                                                                                                                                                                                              414 YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                          61.1%; Score 1536; DB 2; 64.2%; Pred. No. 5.6e-81; ive 59; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                               Ig gamma-2a chain (mAb735) - mouse
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A. Residues: 234-251 < KIM>
A. Residues: 234-251 < KIM>
C. Comment: The a allele sequence is shown.
C. Comment: The a allele sequence is shown.
C. Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds: 1n some cases, such as IgA and IgM, the subunits associate into la C. Superfamily: immunoglobulin c region; immunoglobulin homology
C. Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul F;157-222/pomain: immunoglobulin homology <IM2>
F;157-222/pomain: immunoglobulin homology <IM2>
F;281-350/Domain: immunoglobulin homology <IM2>
F;386-757/Region: hinge
F;386-757/Region: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: interchain (to light chain) #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Rainding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                         A;Title: Sequence of the cloned gene for the constant region of murine gamma2b immunogld
A;Reference number: A26232; WUID:80081502
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamm
     untranslated regions of the murine gamma2b hea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A. Status: 138-161, L',163-189, FP',193-300, R',302-331,'A',333-437,'DI',440-474 <OLL>
A.Cross-references: GB-J00061

R.Kim, H., Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash J. Biol. Chem. 269, 1245-12350, 1994

A.Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A.Reference number: A53598; MUID:94216359
A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                               of gamma2a
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                                                                                                    A; Molecule type: mRNA
A; Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>
A; Note: Lys-474 is probably removed posttranslationally
A; Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: Mouse immunoglobulin allotypes: post-duplication divergence A,Reference number: A26233; MUID:82173203
A,Contents: b allele
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                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 138-172, P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R: Rougeon, F.
Nature 296, 761-763, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.2%; Score 1538; DB 1; Length 4:
61.0%; Pred. No. 4.6e-81;
Live 67; Mismatches 109; Indels
A;Title: Structure of the constant and 3'A;Reference number: A26235; MUID:80081501
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Best Local Similarity
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                                                                                   A; Accession: A26235
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Length 446; Indels

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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Sate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Perin: S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
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                                                                                                                                   A; Molecule type: mRNÅ
A; Residues: 1-470 <SAN>
A; Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
A; Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R; Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A; Title: Structure of bovine immunoglobulin constant region heavy chain (A; Reference number: S06610; MUID:90097956
A; Accession: S06610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 WSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane [F;161-225/Domain: immunoglobulin homology <IMM>
F;161-225/Domain: tamunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                  A; Note: the sequence was determined from the germline
C:Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
                                                                                                                                                                                                                                                                                                               A; Residues: 142-470 <SYM>
A; Residues: references: EMBL:X16701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.43
Best Local Similarity 60.03
Matches 283; Conservative
                                                                  A; Reference number: $22080
A; Accession: $22080
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics
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                                                                                                                                                                                                                 Ig gamma-2b chain precursor - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30.5ep-1989 #sequence_revision 30.5ep-1989 #text_change 23-Jul-1999
C; Accession: 501321
R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a A; Reference number: 501320; MUID:88329081
A; Recession: 501321
A; Molecule type: mRNA
A; Residues: 1-475 < DEL>
A; Molecule type: mRNA
A; Residues: 1-475 < DEL>
A; Note: this sequence was determined from the differentiated gene
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 1-19/Pomain: signal sequence #status predicted <SIG>F; 20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F; 159-223/Domain: immunoglobulin homology <IMM>
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NyAlternate names: Ig gamma-1 chain C region (clone 8.10)
C.Species: Bos primigenius taurus (cattle)
C.Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                           414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GORLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSŞLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V-GLLPFGYWGQGTLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 EEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 KSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.4%; Score 1493.5; DB 2; Length 475; llarity 60.4%; Pred. No. 1.6e-78; Conservative 66; Mismatches 114; Indels 9;
                                                                                       415 KNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 446
                                                                    SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Best Local S
Matches 288
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C; pacies: Homo saplens (man)
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C; Accession: $69339; $72664
R; Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
A; Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A; Reference number: $69339
A; Accession: $6939
A; Accession: $69339
A; Residues: 1-374 KHA>
A; Residues: 1-374 KHA>
A; Residues: 1-374 KHA>
A; Residues: 1-374 KHA>
A; Reference number: $72664
A; Reference number: $72664
A; Redrence number: $72664
A; Recession: $72664
A; Residues: 1-140, C', 142-374 KH2>
A; Cross-references: EMBL:X81695
C; Superfamily: Immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                           347
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                                       NYNOKFKGKATLIVDTSASTAYMELSSLRSEDTAVYYCARNRDYSNNWYF -- DVWGEGTL 135
                                                                                                                                                  VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CP 253
                                                                                                                                                                                                                                                                                               254 APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 RLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARN-RDY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 181
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                                                             CSTLLLIPSWVLSQITLKESGPTLVKPTQTLTLTCTFSGFSLSKSGVGVGWIRQPPGQ
                                                                                                                           VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 CIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTF--TSYWMQWVKQAPGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 374;
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59.7%; Pred. No. 6.9e-75;
ive 29; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain V region precursor - human Species: Homo sapiens (man)
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Matches 280;
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R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porph A;Reference number: JCS810; MUID:98063277
A;Accession: PC4436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed
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C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSHAFAYASYDFWGPGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEPRSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 297
                                                                                                                                                                                                                                                                                                                                                                                   RLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRDYS 122
                                                                                                                                                                                                                                                                                                                                                                                                       TISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYK 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNWYF-----DVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 357
                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: immunoglobulin C région; immunoglobulin homology F;251-320/Domain: immunoglobulin homology <IMM> F;22/Disulfide bonds: interchain (to 98) #status predicted F;99/Disulfide bonds: interchain (to 109) #status predicted
                                                                                                        homology
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A; Residues: 1-472 <PAT>
A; Residues: 1-472 <PAT>
A; Cross-references: EMBL:X69797
C; Superfamily: Immunoglobulin C region; immunoglobulin C; Keywords: immunoglobulin
F; 277-346/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibody 13-1 heavy chain - mouse (fragment)
                                                                                                                                                                                                             ; Score 1466; DB 2; I; Pred. No. 6e-77; 67; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93;
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81; Mismatches 93
                                                                                                                                                                                                                58.3%;
                                                                                                                                                                                                                                 Local Similarity 59.49 Tocal Similarity 59.49
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                   A; Status: preliminary
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Best Local S
Matches 282
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  A; Accession:
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69.6%;
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Best Local Similarity 69.6%
Matches 231; Conservative
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147159
IG gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 *sequence_revision 21-Feb-1997 *text_change 21-Jan-2000
         241
                                                                                                             C. Accession: 147159
R.Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A.Title: Five putative subclasses of swine IgG identified from the CDNA seq A.Title: Five putative subclasses of swine IgG identified from the CDNA seq A.Title: Five putative subclasses of swine IgG identified from the CDNA seq A.Tatle: Five putative subclasses of swine IgG identified from the CDNA seq A.Tatle: Five putative subclasses of swine IgG identified from the CDNA seq A.Tatle: Preliminary translated from GB/EMBL/DDBJ
A.Rolecule type: mRNA
A.Status: 1328 <KAC>
A.Status: BMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
A.Conetics:
A.Genetics:
                                                    ------EPK 145
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                                                                                      SCDKTHTCPPCPAPELLGGPSVFLFPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
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69.9%; Pred. No. 9.8e-66;
Live 42; Mismatches 52;
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sednences Ig gamma 2b chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 147160
B;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from the cDNA sequenc A;Reference number: 147158; MUID:95015845
A;Attle: Five putative subclasses of Swine IgG identified from the cDNA sequenc A;Reference number: 147158; MUID:95015845
A;Accession: 147160
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mARA
A;Residues: 1-328
A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
C;Genetics:
A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology 5 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200 260 Gaps 9 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQ - - PENNYKTTPPVLDSDGSFFLYSKLTVDKS 9 Length 328; Indels ; Score 1261; DB 2; ; Pred. No. 2.2e-65; 41; Mismatches 54; RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

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HV1G_HUMAN HV13_MOUSE HV13_MOUSE HV1B_HUMAN HV1C_HUMAN HV50_MOUSE MUC_HUMAN HV03_MOUSE MUC_RABIT MUC_RABIT MUC_RABIT

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
April 24, 2002, 15:13:46; Search time 29.21 Seconds
(without alignments)
589.951 Million cell updates/sec
2515
Sequence:
1068-09-499-662-89
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059
Minimum DB seq length: 0
Maximum Match 100%
Post-processing: Minimum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_39:*

Database :

	Description	homo sa	P01859 homo sapien	homod	oryct	~	0 homo s	<u> </u>	P22436 mus musculu	P01868 mus musculu	P20761 rattus norv	P01869 mus musculu	P03987 mus musculu	P01863 mus musculu	P20762 rattus norv	P01864 mus musculu	P01865 mus musculu	P20760 rattus norv	P01866 mus musculu	P01867 mus musculu	P01751 mus musculu	mus	P01755 mus musculu	80 mus	snw 61	P01746 mus musculu	3	P01855 rattus norv	4 homo	74	\sim	10	75	P06336 mus musculu
SUMMARIES	ID	GC1_HUMAN	GC2_HUMAN	GC4_HUMAN	GC_RABIT	GC2_CAVPO	GC3_HUMAN	GC1_RAT	GC3_MOUSE	GC1_MOUSE	GCB_RAT	GC1M_MOUSE	GC3M_MOUSE	GCAA_MOUSE	GCC_RAT	GCAB_MOUSE	GCAM_MOUSE	GCA_RAT	GCB_MOUSE	GCBM_MOUSE	HV07_MOUSE	HV06_MOUSE	HV11_MOUSE	HV48_MOUSE	HV05_MOUSE	HV02_MOUSE	HV09_MOUSE	EPC_RAT	EPC_HUMAN	HV04_MOUSE	HV49_MOUSE	HV15_MOUSE	HV10_MOUSE	EPC_MOUSE
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	Score	1758	1610	1599.5	1231.5	1210.5	1162	1155	1150	1145	1144.5	1140	1139	1129	1127.5	1126.5	1124	1115	1085	1080	551.5	520	513.5	513	208	499	496	486.5	486	483	480	-	474	471
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                                                                                                                                                                                                                                                   Dreker L., Schwarz J., Reichel W., Hilschmann N.;

Rule of antibody structure. The primary structure of a monoclonal [761 immunoglobulin (mysloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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K -> R (IN GIM(3) MARKER).

/FTId-VAR_003886.

D -> E (IN GIM(NON-1) MARKER).

/FTId=VAR_003887.

L -> M (IN GIM(NON-1) MARKER).

/FTId=VAR_003888.
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INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
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                                                                         MEDLINE=77070267; PubMed=1002129;
                      iochemistry 9:3188-3196(1970).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM0407; IGcl; 2.
SMART; SM0410; IG_like; 1.
PROSITE; PS00299; IG_MHC; 2.
   Intrachain disulfide bonds.";
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PDB; 1FC2; 15-JUL-92.
MIM; 147100; -
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 238-275 (ZIE).

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"A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains.";
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                                                                                                                                                                                                                                                      Wang A.-C., Tung E., Fudenberg H.H.;
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J. Immunol. 125:1048-1054(1980).
                                                                                                                                        heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS TO 25; 59; 60 AND 264-268 (ZIE). Hofmann T., Parr D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1980) to the PIR data bank
                                                                                                                                                                                                          SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL). MEDLINE=81007873; PubMed=6774012;
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MEDLINE-69064124; PubMed-5782707;
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Interpro; IPR003597; Ig_Cl.
Interpro; IPR003600; Ig_like.
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NCBI_TaxID=9606;
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MEDDIINE-70207560; PubMed=4192699;
Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.";
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S -> A (IN MYELOMA PROTEINS TIL & ZIE).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BIDILINE=83157104; PubMed=6299662;
Ellison J.W., Buxbaum J.N., Hood L.E.;
"Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
DNA 1:11-18(1981).
                                                                                     CHAIN).
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                                                           INTERCHAIN (WITH A LIGHT CHAIN)
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20-JUL-1986 (Rel. 04), Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
Fdam; PF00047; Ig, 3.
SMART; SM00407; IgC1; 2.
SMART; SM00410; IG_11ke; 1.
PROSITE; PS00290; IG_MHC; 2.
J. 117:33-47(1970).
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                                                                                                       MEDLINE-84030930; PubMed-6313520;
Bernstein K.E., Alexander C.B., Mage R.G.;
"Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
                                                                                                                                                                                                                                      SEQUENCE OF 1-128.
MEDIINE-76135469; Pubwed=1243651;
Pratt D.M., Mole L.E.,
"Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype.";
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 88-266 FROM N.A.
SEQUENCE OF 88-266 FROM N.A.
SEQUENCE 829917; PubMed-6193512;
Matters C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
Matters C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit 1gG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D11 AND E15
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEJ.
SEQUENCE OF 132-161.
MEDLINE-70110015; PubMed-5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit 'mmunnalohulin G.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STOCKHOLM (1907).
-1- MISCELLANDOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND
MARKERS AND REF.5 THE E15 MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 129-131 AND 155-322.
Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.);
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I REF. 3 AND 4).
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A (IN EEF. 2).

E (IN REF. 2).

E (IN REF. 3 AND 4).

D (IN REF. 5).

E (IN REF. 5).

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InterPro; IPR003597; Ig_cl.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGcl. 2.
PROSITE; PS00290; IG_MHC; I.
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                                       NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure of heavy chain from strain 13 guinea pig immunoglobulin G(2). II. Amino acid sequence of the carboxyl-terminal and hinge region cyanogen bromide fragments.";
                                                                                                                                                                                                                                   SLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSV 263
                                                                                                                 Gaps
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MEDLINE=71058471; PubMed=5538606;
Birshtein B.K., Hussain Q.Z., Cebra J.J.;
Structure of heavy chain from strain 13 quinea pig
immunoglobulin-G(2). 3. Amino acid sequence of the region around the half-cystine joining heavy and light chains.";
Biochemistry 10:18-25(1971).
                                                                                                                                                                                        4 KAPSVFPLAPCCGDTPSSTVTLGCLVKGYLPEPVTVTWNSGTLTNGVRTFPSVRQSSGLY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-75036072; PubMed-4429665;
Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 homology region from guinea pig IgG2
antibodies.";
                                                                                                                                                                                                                                                                                                                                                                                                            Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                 7;
                                                                             DB 1; Length 323;
                                                                                                                 57; Indels
  284 N -> S (IN REF. 5).
35404 MW; 69E8AA118D579A8B CRC64;
                                                                         b; Score 1231.5; DB
b; Pred. No. 1.4e-78;
34; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G GAMMA-2 CHAIN C REGION.
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Submitted (APR-1975) to the PIR data bank,
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MEDLINE=71058486; PubMed=5538616;
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                                                                           49.0%;
70.0%;
                                                                                                               Matches 229; Conservative
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  284
284 2
323 AA;
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SEQUENCE OF 134-226.
                                                                                           Similarity
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P01862;
CONFLICT
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DT C2_1-JUI

DT 21-JUI

EGAL

COX Mamman

OX NCBL.

RN ISCOUE

RN Triscl

RN SEQUE

RN BIRCHI

RN HILL

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Biochemistry 10:26-31(1971).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN 13 INBRED GUINEA PIGS.
                                                                                                                                  DISULFIDE BONDS.
MEDLINE-71058474; PubMed-4922544;
Oliveira B., Lamm M.E.;
"Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435
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SEQUENCE OF 227-311.

BEDLINE-75036073. PubMed-4609467;

Trischmann T.M., Cebra J.J.;

"Primary structure of the CH3 homology region from guinea pig 19G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318 QYNSTYRVVSVLIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLTV
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P01860, 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
IG GAMMA-3 CHAIN C REGION (HEAVY CHAIN DISEASE PROTEIN) (HDC).
IGHG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.1%; Score 1210.5; DB 1; Length 329; 69.8%; Pred. No. 4.2e-77; cive 30; Mismatches 62; Indels 9;
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                            Biochemistry 13:4804-4811(1974)
                                                                                                                                                                                                                                                                                        Interpro; IPR003006; Ig_MHC.
Interpro; IPR003509; Ig_cl.
Interpro; IPR003500; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGCl; 2.
SWART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
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nes 233; Conservative
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178
248
329 AA;
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Brueggemann M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND ALLO F THE CHI REGION.

INSCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION AND ALLO F THE CHI REGION.

INSCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL GAMMA-3 HEAVY CHAINS.

INSCELLANEOUS: DISEASE PROTEIN OWN MAY REPRESENT AN ALLELIC FORM OR ANOTHER GAMMA CHAIN SUBCLASS.

INSCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR TIMES AS LONG AS IN OTHER GAMMA CHAINS SHOWN CHAINS AND CONTAINS THREE SEGMENT (12-28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
-!- SUBUNT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
NORMALLY PRESENT IN THE HINGE REGION.
-!- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
-!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
                                                                      SEQUENCE (DISEASE PROTEIN WIS).
MEDLINE-61021548; PubMed-6774747;
Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
"Primary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis.";
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-82247835; PubMed-6808505;
Alexander A., Steinmetz M., Barritault D., Frangione B.,
Franklin E.C., Hood L., Buxbaum J.N.;
"Gamma Heavy chain disease in man: cDNA sequence supports partial
                                                                                                                                                                                        MEDLINE-77118561; PubMed-402363; Michaelsen T.E., Frangione B., Franklin E.C.; Primary structure of the 'hinge' region of human 1gG3. Probable quadruplication of a 15-amino acid residue basic unit.";
                                                                                                                                                                                                                                                                                            MEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Frangione B., Prelli F., Franklin B.C.; Withe amino acid sequence of Theavy chain disease' protein ZUC Structure of the Fc fragment of immunoglobulin G3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain; Immunoglobulin C region; Glycoprotein.
Think HINGE.
Think CH2.
Think CH2.
                                                                                                                                                                                                                                                                                REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
                                                                                                                                                                                                                                                                                                                                                        Blochem. Biophys. Res. Commun. 71:907-914(1976).
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
                                                                                                                                                                             REVISIONS TO 12-97 OF PROTEIN WIS.
                                                                                                                                                                                                                                                     J. Biol. Chem. 252:883-889(1977).
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                                                                                                                                               Biochemistry 19:4304-4308(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Ig; 2.
SMART: SM00407; IGC1; 1.
SMART: SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
 sapiens (Human)
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MIM; 147120; -.
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239 EPRSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
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Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
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tive 11; Mismatches 9; Indels
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E69CBC95705B2F46 CRC64;
                                                                                            HEAVY
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T -> A (IN OMM).
/FTIG-VAR_003893.
S -> N (IN OMM).
                                                                                                                                                                                                                                                                                                                                                                                                                QV -> EB (IN 2UC)
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F -> Y (IN OMM).
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FUL-1999 (Rel. 38, Last annotation update)
IG GAMMA-1 CHAIN C REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> T (IN OWM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> Y (IN OMM
                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VAR_C
P -> T
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MEDLINE-89232738; PubMed-3149946;
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140
290
127
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Mammalia; Eutheria;
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139
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MOD_RES
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P20759;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                  F45827174182BAD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) IG GAMMA-1 CHAIN C REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 AA
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                                                                                                                                                                                                                                          Alternative splicing
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HINGE.
CH2.
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                                                                                                                EMBL; J00451; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                        CH3
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                                                                                                                                      InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_cl.
InterPro; IPR00360); Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGcl; 2.
SMART; SM00407; IGcl; 2.
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223 CF
327 CF
3628 MW;
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                                                                                                                              PIR; B02156; G3MSC
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P01868;
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SEQUENCE
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"Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988).
PIR: PS0017; PS0017; PS0017: InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_cl.
                                                                                                                                                                                                                                                                                                                                                                   141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                  60 GLYTLTSSVIVPSSTWPSQTVTCNVAHPASSTKVDKKIVPRNCG--GDCKPC----ICTG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 SEVSSVFIFPPRARDVLTITLTPRVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (POTENTIAL).
013BAB45EF49B9DA CRC64;
                                                                                                                                                                                                                                                                                                                  45.9%; Score 1155; DB 1; Length 326;
63.4%; Pred. No. 3e-73;
.ive 52; Mismatches 60; Indels 10;
                                                           INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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MEDLINE=85027161; PubMed=6092053;
Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
6 AAMAA-3 CHAIN C REGION, SECRETED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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HINGE.
CH2.
CH3.
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                                                                                                                                                                                                                                                                              35946 MW;
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Best Local Similarity 63.49
Matches 211; Conservative
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219
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140
246
176
326 &
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1113
220
27
102
106
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P22436;
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DOMAIN
DISULFID
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GC3_MOUSE
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                                                                                                                                              202 LYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP--PCPAPELLG 259
                                                                                                                                                                   60 FYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-IPKPSTPPGSSCPPGNILG 118
                                                                                                                                                                                                                       GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319
                                                                                                                                                                                                                                          NSTYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE 379
                                                                                                                                                                                                                                                                                                                EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 439
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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45.7%; Score 1150; DB 1; Length 329;
65.0%; Pred. No. 6.7e-73;
Live 44; Mismatches 68; Indels
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35704 MW; A338812F3D1F2C93 CRC64;

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324 AA;
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DISULFID
  SEQUENCE
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Best Local $
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P20761;
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                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                      SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDILINE-80012837, PubMed-113776;
RSOgers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                  SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
MEDIANE-80202559; PubMed=6769752;
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Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immutoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
           Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                        "The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850(1972).
                                                                                                                                                                                                                                    Adetugbo K.;
"Evolution of immunoglobulin subclasses. Primary structure of
murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlycoSuiteDB, P01868; --
MGD, MGI:96446; Igh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
Pfam; PF000147; ig, 3.
SWART; SW00407; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
NON_IER
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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D (IN REF. 3).
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                                                                                                                                                                                             Nucleic Acids Res. 6:3305-3321(1979).
                                                                                                                                                                                                                SEQUENCE (MYELOMA PROTEIN MOPC 21).
MEDLINE-78242288; PubMed-98524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ^ ^
                                                                                                                                                                                                                                                                                         DISULFIDE BONDS (MOPC 21).
MEDLINE-73008889; PubMed-5073237;
Svasti J., Milstein C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; V00793; CAA24172.1; -. EMBL; V00793; CAA24173.1; -. EMBL; V00793; CAA24174.1; -. EMBL; V00795; CAA24175.1; -.
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217
324
82
102
104
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324
276
278
                    gamma 1 chain gene.";
Cell 18:559-568(1979).
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                                                                                                                                                                                   chain
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Brieggamann M.;

Evolution of the rat immunoglobulin gamma heavy-chain gene family.";

Gene 74.473.482(1988).

PIR; PS0018; PS0018.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003507; Ig_cl.

InterPro; IPR003606; Ig_like.

Ffam; PF00047; Igc. 1.

SMART; SM00407; Igc. 2.

SMART; SM00410; IC_like; 1.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                       115 --SSVEIFPPREMENDVLITLTPRVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                            141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                           201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
                                                                                                                                                                                                                                   319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                       Gaps
                                                                                                                                 1 AKTIPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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     Length 324;
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45.5%; Score 1145; DB 1;
62.3%; Pred. No. 1.5e-72;
ive 55; Mismatches 60;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-5-UL-1999 (Rel. 38, Last annotation update)
IG GAMMA-2B CHAIN C REGION.
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                                                    Matches 207; Conservative
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333 AA;
                             Similarity
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Best Local Similarity
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MEDLINE-8222190; Pubmed-6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;

Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

- ALPERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
                                                                                 60 GLYTLTSSVT--SSTWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCPTCPTCPTCHKCPV 117
                                                                                                                              141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 314
                                                                                                                                                                                                             PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 434
                                                                    GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS-----CDKTHTCPPCPA 254
                                                                                                                                                                REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 374
                                                                                                                                                                                                                       238 GPPTEQLIEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKLN 297
   Gaps
                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
"Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O., "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
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Cell 26:19-27(1981).
 68; Indels
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30-MAY-2000 (Rel. 39, Last annotation update)
IG GAWWA-1 CHAIN C REGION, MEMBRANE-BOUND FORM.
Mus musculus (Mouse).
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 Mismatches
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SEQUENCE OF 323-393 FROM N.A.
MEDLINE-82197626; PubMed-6804950;
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MEDLINE-82115295; Pubmed=6799207;
Rogers J., Choi E., Souza L., Car'
Eisenberg D., Wall R.;
 45;
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 Conservative
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214;
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P01869;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the BNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an emmall to license@isb-sib.ch).
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BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCOD: IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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Alternative splicing; Transmembrane.
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CHAIN).
CHAIN).
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CYTOPLASMIC (POTENTIAL).
4CC88343B7A1CE27 CRC64;
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HINGE.
                                                                                                                                                                                                                                                        EMBL; V00793; CAA24172.1; --
EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
EMBL; V00793; CAA24174.1; --
PIR; BO2159; GIMSM.
MGD; MGI:96446; Igh-4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
Pfam; PF00047; Ig 3
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
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3217
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340
358
393 AA;
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119 GPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREAQY 178
                                       Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10090;
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P01863;
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                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=85027161; Pubmed=6092053;
Wels J.A. Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
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Pred. No. 4.9e-72;
I; Mismatches 68;
                                                                            -JUL-1999 (Rel. 38, Last annotation update) GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM
 398 AA.
                                                        Last sequence update)
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POTENTIAL.
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HINGE.
 PRT;
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EMBL; V01526; CAA24767.1; ALT_SEQ.
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InterPro; IPR003509; Ig_c1.
InterPro; IPR003509; Ig_like.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1; 2.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; 1.
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                                   23-OCT-1986 (Rel. 02, 01-AUG-1991 (Rel. 19,
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388
398 AA;
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Matches 213;
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                                       MEDLINE-81223894; PubMed-6787604; Ollo R., Auffray C., Morchamps C., Rougeon F.; Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes suggests that exons can be exchanged between genes in a multigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-81076554; PubMed-6777755; SiQUENCE FROM N.A. Sikorav J.-L., Auffray C., Rougeon F.; Sixorav J.-L., Auffray C., Rougeon F.; Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA."; Nucleic Acids Res. 8:3143-3155(1980).
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Yamawaki Kataoka Y., Miyata T., Honjo T.;
"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
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"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
Eur. J. Biochem. 43:423-435(1974).
EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
1G GAMMA-2A CHAIN C REGION, A ALLELE.
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Mammalia; Eutheria; Rodentia;
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21-JUL-1986 (Rel. 01, Last Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G GAMMA-2A CHAIN C REGION, B ALLELE.
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InterPro: IPR003006; Ig_MHC.
InterPro: IPR003569; Ig_C1.
InterPro: IPR003560; Ig_like.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IG_1; 2.
SMART; SM00410; IG_like; 1.
PROSITE; PS00299; IG_MHC; 1.
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329 AA;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1G GAMMA-2C CHAIN C REGION.
Eattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1129; DB 1; Length 3 Pred. No. 1.9e-71; 3; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region.
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                                                                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
Fdam; PF00047; Ig; 3.
SMART; SM00407; IGcl; 2.
SMART; SM00410; IG_like; 1.
PROSITE; PS00299; IG_MHC; 1.
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                                   EMBL; V00798; CAA24178.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                7;
                                                                                                                                                                          44.8%; Score 1127.5; DB 1; Length 329; 62.8%; Pred. No. 2.4e-71; Live 51; Mismatches 66; Indels 7;
                                      CHAIN).
INTERCHAIN (WITH A LIGHT CHAIN).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dognin M.J., Lauwereys M., Strosberg A.D.;
Multiple amino acid substitutions between murine gamma 2a heavy
chain Fc regions of 191a and 191b allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                              MEDILINE-82037861; PubMed-6170065; Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.; Multiple differences between the nucleic acid sequences of the IQC2aa and IgG2ab alleles of the mouse."; Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
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44.8%; Score 1126.5; DB 1; Length 335;
Best Local Similarity 61.6%; Pred. No. 2.9e-71;
Matches 207; Conservative 52; Mismatches 70; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER 1 1
SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; PR00047; Ig_13; 3.
SMART; SM00407; IG_11, 2.
SMART; SM004107; IG_11, 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region.
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                                                                                                                                                                MEDLINE-8203777; PubMed-6794027;
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Search completed: April 24, 2002, 15:13:47 Job time: 324 sec

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OM protein - protein search, using sw model

Run on:

April 24, 2002, 15:13:10; Search time 86.76 Seconds
(without alignments)
792.393 Million cell updates/sec
Title:

US-09-499-662-89
Perfect Score:
2515
Sequence:
1 MGWSCIILFLVATATGVHSQ......MHEALHNHYTQKSLSLSPGK 470
Scoring table: BLOSUMG2

Scoring table: BLOSUMG2
Gapop 10.0 , Gapext 0.5
Searched:
473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters:
473505
Minimum DB seq length: 0
Maximum Antoh 0%
Maximum Match 10%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_virus:* sp_vertebrate:*

sp_rodent:*

sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*

sp_archea:*
sp_bacteria:*
sp_fungi:*

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sp_organelle:*
sp_phage:*
sp_plant:*

Result Ouery No. Score Match Length DB ID Description 2 1617.5 64.8 473 11 099624 099124 musculu 2 1617.5 62.7 473 11 099424 099125 mus musculu 4 1551 62.7 473 11 099424 099125 mus musculu 5 1440.5 57.3 437 11 099424 099131 mus musculu 6 846 33.6 500 4 098404 099131 mus musculu 7 751.5 29.9 597 4 098410 099146 mus musculu 9 747.5 29.7 597 4 098410 09948 mus musculu 9 747.5 29.0 487 11 099484 09948 mus musculu 10 728.5 29.0 487 11 099424 09948 mus musculu 11 650.2 23.9 426 11 099422 09948 mus musculu 12 602 23.9 426 11 099429 099420 mus musculu 13 569.5 22.6 416 4 098799 099679 mus musculu 14 509 20.2 150 4 4 099799 099579 mus musculu 15 492 19.6 157 4 099799 095978 mus capien 16 480.5 19.1 384 4 099060 099450 mus musculu 18 454 18.1 11 11 099479 099470 mus musculu 18 451 18.1 117 11 099479 099450 mus musculu 19 452.5 18.0 124 4 099050 099450 mus musculu 19 452.5 18.0 124 4 099050 099450 mus musculu 19 452.5 18.0 124 4 099050 099450 mus musculu 19 452.5 18.0 124 4 099050 099450 mus musculu 19 452.5 18.0 124 4 099050

Q9gyz2 schistosoma Q9u195 homo sapien O9cve9 mus musculu	O921c4 mus musculu O921c4 mus musculu O90189 homo sapien		Q9j177 mus musculu	Q9d9b8 mus musculu	Q9j175 mus musculu	Q9z1c6 mus musculu	Q9bsz1 homo sapien	Q90544 ginglymosto	Q9j183 mus musculu	Q9qyf0 mus musculu		Q9j185 mus musculu	Q9ul90 homo sapien	Q9ul71 homo sapien	Q9u191 homo sapien	Q9u188 homo sapien	homo	homo	Q9ul93 homo sapien	Q9ul72 homo sapien	095973 homo sapien
Q9GYZ2 Q9UL95 Q9OXE9	Q9Z1C4 Q9Z1C4 Q9UL89	Q9JL81	Q9JL77	0909в8	Q9JL75	Q9Z1C6	Q9BS21	090544	09JL83	Q9QYF0	Q9BUA1	Q9JL85	09UL90	Q9UL71	O9UL91	09ur88	09нсс1	Q9UL84	Q9UL93	Q9UL72	095973
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119	118	114	110	111	109	117	375	684	110	298	120	109	113	121	118	131	112	122	116	118	150
17.7	17.2	17.1	16.9	16.3	16.2	15.9	15.9	15.7	15.0	14.5	14.3	13.8	12.9	12.6	12.5	12.5	12.4	12.2	12.2	11.9	11.7
444 444 444	433.5	429.5	428.5	409	407.5	399	399	396	377.5	363.5	359	348	325	316	315.5	315	312.5	307.5	306	298.5	294.5
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ALIGNMENTS

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61 GORLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120
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                                                                                   GORLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                       121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS
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Ol-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
Mus muscalus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutherala; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                            WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.; Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003888; AAH03888.1; -. SPOUTENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
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Best Local 9
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                          DB 11; Length 473;
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                                                                                                                                                                         Query Match 64.8%; Score 1628.5; DB 11; Lengt
Best Local Similarity 63.4%; Pred. No. 1.7e-125;
Matches 302; Conservative 70; Mismatches 95; Indels
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003435; AAH03435.1; -.
SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;
                                                                                                                    IG_MHC; UNKNOWN_1.
51699 MW; 9DED57A514475FBB CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
Mus musculus (Mouse).
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
        InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_like.
InterPro; IPR003506; Ig_MHC.
Pfam: PF00047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00406; IG; 3.
SMART; SM00406; IG; 1.
SMART; SM00410; IG_like; 1.
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 KSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1551; DB 11; Length
Pred. No. 3.8e-119;
62; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC003878; AAH03878.1; -. SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
SIMILAR TO RIKEN CDNA 1810060009 GENE.
                                                                                                                                                                                                                                                                                                                                                                        468
                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.78;
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Best Local Similarity 62.55
Matches 295; Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S., "Cloning of CDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 DSVKGRPTIYKDKDRNILSLQMSSLRSEDTAMYYCARG-DYS----AYWGPGTLVTVSA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LYTLSSSYTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCICTVPEV- 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 VQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQRLEWMGEIDPSDSYTNYN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SSVFIFPFREKOVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
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                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 11; Length 437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.3%; Score 1440.5; DB 11; Lengt
59.3%; Pred. No. 4.1e-110;
.ive 72; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5C3A7BB3EE7D697C CRC64;
                                                 Created)
Last sequence update)
Last annotation update)
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       437
O9R1A4 PRELIMINARY; PRT; 43
O9R1A4;
01-MAY-2000 (TYEMBLYEL: 13, Created)
01-MAY-2000 (TYEMBLYEL: 13, Last sequen
01-UIN-2001 (TYEMBLYEL: 17, Last annota
GAMMA1 HEAVY CHAIN OF WAB7 (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF152372; AAD40243.1; -.
HSSP; P01842; 7FAB.
INTERPLO; IPR003600; Ig_like.
INTERPRO; IPR003606; Ig_MC.
INTERPRO; IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IG_V: 1.
SMART; SM00410; IG_like; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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437 AA;
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17;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            Matches 180; Conservative
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                                                               Submitted (FEB-2001) to EMBL; BC002963; AAH0296
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TISSUE-MAMMARY TUMOR;
                                                                                                                                  Similarity
                               SEQUENCE FROM N.A.
TISSUE-LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10090;
         NCBI_TaxID-9606;
                                                     Strausberg R.;
                                                                                      SEQUENCE
                                                                                                                       Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                              120 DYS----NNWYF----DVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 NTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPK--------DTLM 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPSQDVTV------PCPVPSTPPTPSPST-PPTPSPSCCHPRLSLHRPALEDLL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 WLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKG 394
                                                                                                                                                                                                                                                                                                    1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BUIO;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN (PROTEIN FOR MGC:1652).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                             Length 500;
                                                                                                                                                                                                                                          33.6%; Score 846; DB 4; Length 50
40.7%; Pred. No. 3e-61;
Live 68; Mismatches 179; Indels
                                                                                                                                                                                      (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                          Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ database
EMBL; BC005951; AAH05951.1; -.
SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:14588).
HOMO sapiens (Human).
                              500 AA
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                              PRT;
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VGHEALPLAFTQETIDRLAGK 482
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                              PRELIMINARY;
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                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                   TISSUE-PROSTATE;
                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                  204;
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Best Local S
                             Q9BRV0
                                          Q9BRV0
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Q9BRV0
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GEIDPSDSYTWYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCAR-----NRDYS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VFLFPPKFKDTLAISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPSRE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMT-KNOVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDGSFFLYSKLT 434
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                8 LFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQRLEWM 67
                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                              GRYGMDVWGQGTTVTVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 NNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROFIEIN PR MGC:6319).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHKPSN----
                                                                                                                                                                             Indels 117;
                                                                                                                           Length 597;
the EMBL/GenBank/DDBJ databases
                        2963; AAH02963.1; -.
597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -PCPAPELLGGPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----TKVDKRVEPKS------CDKTHTCP----
                                                                                                           29 9%; Score . 2.1e-c...
31.2%; Pred. No. 2.1e-c...
...e 91; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484 AA
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us-09-499-662-89.rspt

17;

Gaps

117;

Indels

Pred. No. 4.5e-53; L; Mismatches 189;

91;

31.18;

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LFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAPGQRLEWM 67
 Best Local Similarity 31.19
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q99KA4;
                                                                                                                                                                                                                                                                                                                                                                                                                                  099KA4
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099KA4
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                                                        16;
                                                                                                                       GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                 YSNNWY-FDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVT 178
                                                                                                                                                                                     VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKR 237
                                                                                                                                                                                                                                                                                                 IEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLICLVKGFYPSDIAVEWESNGQ---P 410
                                                                                                                                                                                                                                                                                                                                                 FNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
                                                                          9
                                                                                  Gaps
                                                                        1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                          VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                        28;
                                     Length 484;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strauberg R.;
Strauberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006180; AAH06180.1; --
EMBL; BC001872; AAH01872.1; --
SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
BC003495; AAH03495.1; -.
ICE 484 AA; 52567 MW; BEAEA4F9BCF582FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UNKNOWN (PROTEIN FOR MGC:1905) (PROTEIN FOR MGC:1228).
                                    Ouery Match 29.9%; Score 751; DB 11; Best Local Similarity 36.5%; Pred. No. 1.8e-53; Matches 176; Conservative 89; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                           597 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=RHABDOMYOSARCOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LYMPHOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                         GK 470
                                                                                                                                                                                                                                                                                                                                                                                            466
         SEQUENCE
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Query Match

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                                                                                                        GRYGMDYWGQGTTYTYSGSASAPTLFPLYSCENSPSDTSSVAYGCLAQDFLPDSITFSW 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 PLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 DQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCVPDQDTA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --VELFPPRPRDILMISRIPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPSRE 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GORLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARN-- 118
                                                                        68 GEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCAR-----NRDYS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMT-KNOVSLICLVKGFYPSDIAVEWESNGQP--ENNYKTIPPVLD--SDGSFFLYSKLT 434
1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 NNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW
                                                                                                                                                                                                                                                                                                 --NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTOTY-ICNVNHKPSN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNKNOWN (PROTEIN FOR MGC:6727).
Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.0%; Score 728.5; DB 11; Length 487; 35.1%; Pred. No. 1.3e-51; live 89; Mismatches 196; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO04786; AAH04786.1; -.
SEOUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               -----TKVDKRVEPKS------CDKTHTCP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 35.1%
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -PCPAPELLGGPS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 747.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.78;
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18;
177 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVD 235
                                                                                                                                                                                   296 VKFNWYVDGVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALP 352
                                                                                                                                                                                                                                                                                      353 APIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ-- 409
                                                                                                                                                                                                                                                                                                         410 -PENNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 466
                                                                                                                                                                                                                                                                                                                                                                     66 WMGYIN-YDGSNNYNPSLKNRISITRDTSKNQFFLKLMSVTTEDTATYYCA-SRGYS--- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WMGEIDPSDSYTNYNQKFKGKATLIVDISASTAYMELSSLRSEDTAVYYCARNRDYSNNW 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 YFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTVSWNSG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YWMQWVKQAPGQRLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                            -RDYSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-P
                                                                                                                                    MNVTWGKSGKDITTVNFPPALASGGYTMSSQLTLPAVECPEGESVKCSVQH---DSNAV
                                                                                                                                                                                                                                                 293 V-FTW-----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .85 ALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT-QTYICNVNHKPSNTKVDKRVEPKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.0%; Score 653; DB 11; Length 479; 33.8%; Pred. No. 1.9e-45; tive 90; Mismatches 193; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: BC002091; AAH02091.1; -.
SEQUENCE 479 AA; 51992 MW; 768E39A138918892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNKNOWN (PROTEIN FOR MGC:6342).
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Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-MAMMARY TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                              SPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                            466 LSGK 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    099M22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
              61
                                                                                                                                     180
                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                                                                                                                              467
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-C57BL/6J; TISSUE-KIDNEY;

RAMAN ALZAWA T., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAMAN J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAMAN ALZAWA T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A alzawa K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

RA Gadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,

RA Richi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rochrim I. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Schrim I. M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Rama Sakai K., Okido T., Futunon M., Aono H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Rushincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Storch K.H., Weltz C., Whittaker C., Wilming L.,

Nordone P., Marshav-Bootis A., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Nordone P., Marshav-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nordone P., Marshis W.H., Weltz C., Whittaker C.,

Nordone P., Marshav-Bootis A., Wang K.H., Weltz C., Whittaker C.,

Nordone P., Rang B.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i - SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                              289 --EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPE-SGTLTGTIA 345
244 DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 303
                                                                                                           304 GVEVHNAKTKPREEQYNST---YRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
                                                                                                                                                                                                                         361 KAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKT 416
                                                                                                                                                                                                                                                      236 SGPTPPPPITIPSC--QPSLSLQRPALED-LLLGSDASITCTLNGLRNPEGAV-FTW---
                                                                                                                                                                                                                                                                                                                                        417 TPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                        406 EPLKEPGEGATTYLVTSVLRVSAETWKQGDQYSCMVGHEALPMNFTQKTIDRLSGK 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TremBirel. 17, Last sequence update)
01-JUN-2001 (TremBirel. 17, Last annotation update)
ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:0610041A01, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00290; IG_MHC; UNKNOWN_1.
426 AA; 45819 MW; 56E1275BA48F6FB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.9%; Score 602; DB 11; 32.6%; Pred. No. 2.5e-41; ive 75; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK002875; BAB22422.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00409; 1G; 3.
SMART; SM00409; IG; 3.
SMART; SM00410; IGcl; 3.
SMART; SM00410; IGclike; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 23.9
Best Local Similarity 32.6
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:685-690(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9DCD9;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Q9DCD9
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16;

Gaps

84;

Indels

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human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
EMBL, AL38978; CAB97534.1;
-InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469
                                                                                                                                                                                                                                                                                                                                                         121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE-PVTV 179
                                                                                                                                                                                                                                                                                                                                                                                                            63 YYGPYAMDYWGQGTSVTVSSESARNPIIYPLT-LPRALSSDPVIIGCLIHDYFPSGTMNV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 NWYYDGVEVHNAKTKPREEQYNST---YRVVSYLTVLHQDWLNGKEYKCKVSNKALPAPI 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TW----EPSTGKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDT-L
                                                                                                                                                                            GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD
                                                                                                                                                                                                                           :| | | | | | | | :: |:: |:| |:: |:| |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               356 EKTISKAKGOPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYLVFEPLKEPGEGATTYLVTSVLRVSAELWKQGDQYSCMVGHEALPMNFTQKTIDRLSG
MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQWVKQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWNSGALTSGVHTFPAVLQSSGLYSLSSVYTVPSSSLGT-QTYICNVNHKPSNTKVDKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 NNYKTTPPVLDSDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The European IMAGE consortium for integrated Molecular analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K., Lehrach H., Poustka A., Lundeberg J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Pluvinet R., Estivill X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
LIN HEAVY CHAIN VARIANT (FRAGMENT).
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SMART; SMO0406; IGv; 1.

SMART; SMO0410; IG_11ke; 3.

PROSITE; PSO0290; IG_MHC; UNKNOWN_2.

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SEQUENCE 416 AA; 44786 MW; 8C417
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                                                                                        MGFSRIFLFLLSVTTG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606
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SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000
01-OCT-2000
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29NPP6
AC 09NPP6, DT 01-0CT
DT 01-0CT
DT 01-0CT
DT 01-0CT
DT 01-1CT
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17;
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                                                                                                                    60 PGQRLEWMGEIDPSDSYTNYNQKFKGKATLIVDTSASTAYMELSSLRSEDTAVYYCARNR 119
                                                                                                                                                          TVSWNSGALTSGVHTFPAVLQSSG-LYSLSSVVTVPSSSL-GTQTYICNVNH--KPSNTK 233
                                                                                                                                                                                                                                                                 294 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 353
                                                                                                                                                                                                                                                                                                                                                                         411 ENNYKTIPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 467
                                                                                                      DYSNNWY-FDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP-EPV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   study with an patient with
                                                                                                                                                                                                                                                                                                                   PIEKTISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--P
                                                                 -----DVTVPCPVPPPPCC-HPRLSLHRPALED-LLLGSEANLTCTLTGL-RDA
                                                                                                                                                                                                                                                                                 SGATFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAQPWNHGETFTCTAAHPELKT
                                                                                                                                                                                                             VDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                        37;
 Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 150;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563D164AB22802D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
MEDLINE-98322155; Pubwed-9657749;
Jacquemin M.G., Vander Elst L.P.L.;
"Mechanism and kinetics of factor VIII inactivation: sign monocomal antibody derived from a hemophilia A juhihitor.";
Blood 92:496-506(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
IGG VH PROTEIN PRECURSOR (FRAGMENT).
  4
             ; Pred. No. 1.1e-38; 66; Mismatches 172;
 DB
Score 569.5;
Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 509;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.2%;
 Query Match 22.6%;
Best Local Similarity 35.0%;
Matches 148; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
150
16031 N
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150 ::
150 AA;
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TISSUE-PERTPHERAL BLOOD;
JOX A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
Bohlen H., Diehl V., Wolf J.;
Rabsence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
patient with mixed cellularity Hodgkin's disease is associated with
somatic mutations within the untranslated regions of rearranged and
class switch recombinated Ig genes.",
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

I SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
                                                                                                        61 GQRLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                        61 GORLEWMGEIDPSDSYTNYNQKFKGKATLTVDTSASTAYMELSSLRSEDTAVYYCARNRD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGWSCIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMOWVKQAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                   Indels
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157 157
157 AA; 17304 MW; 86986EDDA84D88B5 CRC64;
                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VHI PROTEIN PRECURSOR (FRAGMENT).
Best Local Similarity 66.2%; Pred. No. 2.8e-34;
Matches 100; Conservative 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 61.1%; Pred. No. 7.5e-33;
Matches 96; Conservative 20; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKS 157
                                                                                                                                                                                                                                                                             157 AA.
                                                                                                                                                                   121 YSNNWYFDVWGEGTLVTVSSASTKGPSVFPL 151
                                                                                                                                                                                     PRT;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; I.
SMART; SM00406; IGV; I.
                                                                                                                                                                                                                                                                             PRELIMINARY;
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Search completed: April 24, 2002, 15:13:12 Job time: 290 sec